

P1 1125369

REC'D 20 FEB 2004

WIPO

PCT

THE UNITED STATES OF AMERICA

TO ALL TO WHOM THESE PRESENTS SHALL COME:

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office

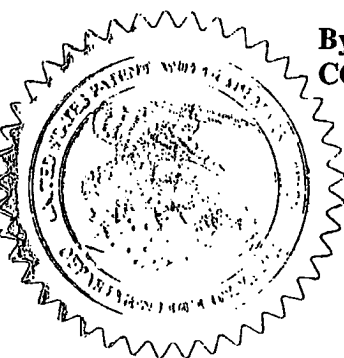
February 11, 2004

THIS IS TO CERTIFY THAT ANNEXED HERETO IS A TRUE COPY FROM THE RECORDS OF THE UNITED STATES PATENT AND TRADEMARK OFFICE OF THOSE PAPERS OF THE BELOW IDENTIFIED PATENT APPLICATION THAT MET THE REQUIREMENTS TO BE GRANTED A FILING DATE.

APPLICATION NUMBER: 60/368,618 —

FILING DATE: March 29, 2002 —

RELATED PCT APPLICATION NUMBER: PCT/US03/08880 —



By Authority of the
COMMISSIONER OF PATENTS AND TRADEMARKS

M. Lee

M. LEE
Certifying Officer

**PRIORITY
DOCUMENT**

SUBMITTED OR TRANSMITTED IN
COMPLIANCE WITH RULE 17.1(a) OR (b)

03/29/02

16369 U.S. PTO

16369 U.S. PTO
03/29/02

84-81-02

Customer Number: 000959

A/ROV
seg wtr

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Yocum, et al.

Attorney
Docket No. BGI-152-3

For: Methods and Organisms for Production of B6 Vitamers

Commissioner for Patents
Box Provisional Patent Application
Washington, D.C. 2023116369 U.S. PTO
60/368618
03/29/02

CERTIFICATION UNDER 37 CFR 1.10

Date of Deposit: March 29, 2002Mailing Label Number: EL 833 314 145 US

I hereby certify that this Cover Sheet for Filing Provisional Application (37 C.F.R. §1.51(2)(i)) and the documents referred to as attached therein are being deposited with the United States Postal Service on the date indicated above in an envelope as "Express Mail Post Office to Addressee" service under 37 CFR 1.10 and addressed to the Commissioner for Patents, Box Provisional Patent Application, Washington, D.C. 20231.

Larry Taylor

Name of Person Mailing Paper


Signature of Person Mailing Paper

COVER SHEET FOR FILING PROVISIONAL PATENT APPLICATION

Dear Sir:

The accompanying application, entitled "Methods and Organisms for Production of B6 Vitamers," is a provisional patent application under 37 C.F.R. §1.51(c) and §1.53(c).

1. ☒ The name(s) and address(es) of the inventor(s) of this application is/are as follows:

1	Yocum	R.	Rogers	4 Orchard Lane, Lexington, Massachusetts 02420
2	Williams	Mark	K.	58 School Street, Revere, Massachusetts 02151
3	Pero	Janice	G.	20 Solomon Pierce Road, Lexington, Massachusetts 02420

2. ☒ The following documents are enclosed:

- ☒ 28 page(s) of Specification
- ☒ 6 page(s) of Claims
- ☒ 1 page(s) of Abstract
- ☒ 12 page(s) of Sequence Listing
- ☒ 7 sheets of Informal Drawings; and
- ☒ Return postcard.

3. ☒ The fee for filing this provisional application, as set forth in 37 CFR 1.16(k), is \$160.00.

a. ☒ A check for this filing fee is enclosed.

b. ☐ Charge the filing fee to Deposit Account No. _____
(A duplicate copy of this sheet is enclosed.)

c. ☐ The filing fee is not being paid at this time.

4. ☒ Please charge any fee deficiencies associated with this filing to Deposit Account No. 12-0080. A duplicate copy of this sheet is enclosed.

5. ☒ Please address all future communications to: **Customer Number: 000959** whose address is:

Lahive & Cockfield, LLP
28 State Street
Boston, MA 02109

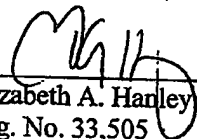
and direct telephone calls to: Elizabeth A. Hanley, (617) 227-7400

Respectfully submitted,

March 29, 2002

Date

LAHIVE & COCKFIELD, LLP
28 State Street
Boston, MA 02109
Tel. (617) 227-7400


Elizabeth A. Hanley Esq.
Reg. No. 33,505
Attorney for Applicants

METHODS AND ORGANISMS FOR PRODUCTION OF B6 VITAMERS

Background of the Invention

5 Vitamin B6, also known as pyridoxine or pyridoxol (PN), or one of a number of closely related compounds, is an essential dietary nutrient for most, if not all, animals, while many micro-organisms (bacteria, fungi, algae, etc.) and plants are capable of synthesizing their own vitamin B6 or compound(s) related to vitamin B6. When an animal ingests PN or a related compound that has vitamin B6 activity, the
10 compound is converted ultimately into pyridoxal phosphate (PLP) and/or pyridoxamine phosphate (PMP), which are the active forms of vitamin B6 in all living organisms. PLP acts as a cofactor for many important or essential enzymes in all living organisms, including transaminases, racemases, and decarboxylases. PLP and PMP are easily interconverted by ubiquitous transaminases.

15 Vitamin B6 is of commercial importance in vitamin pills, pharmaceutical applications, and as an animal feed additive that enhances growth or desirable growth characteristics in farm and domestic animals. The currently used commercial process for producing vitamin B6 is a synthetic chemical process. However, a fermentation process using a microorganism (see US Patent application No. 09/667,569, filed
20 September 21, 2000, hereby incorporated in its entirety by reference) or a biosynthetic process using a plant species can be more cost effective in the long run, and may be environmentally more attractive.

The biosynthetic pathway for PLP in *E. coli* has been elucidated (reviewed in Mittengruber, G., (2001) *J. Mol. Microbiol. Biotechnol.* 3(1): 1-20; Cane, D.E., et al. (2000) *J. Am. Chem. Soc.* 122: 4213-4214; Man, T-K, et al., (1996) *J. Bacteriol.* 178: 2445-2449). Enzymes encoded by the genes *epd*, *pdxB*, *pdxF*, and *pdxA* lead to synthesis of the precursor 1-hydroxy-3-amino acetone phosphate from erythrose-4-phosphate and glutamate. The enzyme encoded by *dxs* leads to the precursor 5'-deoxyxylulose phosphate from glycolytic intermediates. The enzyme encoded by *pdxJ*
30 then catalyzes the chemical coupling of the two precursors to give pyridoxol phosphate (also called pyridoxine phosphate or PNP). PNP is then oxidized to the active form, PLP, by the enzyme encoded by *pdxH*. This biosynthetic pathway to PLP in *E. coli*, as well as closely related pathways, are referred to herein as the Type A Pathway. Partially characterized mutants of *E. coli* have been described that produce about three- to seven-
35 fold more vitamin B6-related compounds than the parent strain (Dempsey and Arcement (1971) *J. Bacteriol.* 107(2): 580-582). Partially characterized mutants of *B. subtilis* have been reported that produce 1 - 5 mg/l vitamin B6, but it was not stated what level the

50368618-032900

parent strain produced (Pflug, W., and Lingens, F., (1978) Hoppe-Seyler's Z. Physiol. Chem. 359: 559-570). Notably, these organisms were not recombinantly produced.

A second biosynthetic pathway for vitamin B6, referred to herein as the Type B pathway, may exist in some organisms other than *E. coli* (Mittengruber, G.,
5 (2001) *J. Mol. Microbiol. Biotechnol.* 3(1):1-20). In particular, some fungi (for example from the genera *Cercospora*, *Neurospora*, *Aspergillus* and *Saccharomyces*), some bacteria (for example *B. subtilis* and *Staphylococcus aureus*), and all plants for which data exists do not contain any genes that are highly homologous to *E. coli* *pdxA* and *pdxJ*. Instead, these organisms contain genes that are homologous to *Cercospora* genes
10 named *SOR* (or *SNZ*) and *SNO*. In *Saccharomyces*, these homologs are called *PDX1* and *PDX2*, respectively, and in *B. subtilis*, these homologs are named *yaaD* and *yaaE*, respectively. In *B. subtilis*, there have been no reports as to whether *yaaD* or *yaaE* are actually involved in PLP biosynthesis. Protein or DNA sequence homology alone is not sufficient to establish biological function. For example, *B. subtilis* contains a gene,
15 *yhaF*, that encodes a protein that is significantly homologous to *E. coli* *pdxF*. However, when *yhaF* is mutated, the resulting mutant *B. subtilis* strain is a serine auxotroph, but not a PL auxotroph (see Example 3, below). Thus, the identification of a gene or genes involved in PLP biosynthesis in any given organism can not be done using sequence homology alone.

20 Results from ¹³C and ¹⁵N labeling studies suggest that the precursors that provide the carbon and nitrogen atoms in PL and related compounds are different in *E. coli* and *Saccharomyces cerevisiae* (Gupta, R., et al. (2001) *J. Am Chem. Soc.* 123: 11353-11359; Tayuza, K., et al. (1995) *Biochim. Biophys. Acta* 1244: 113-116.) However, the identity of the precursors for PL and related compounds in *S. cerevisiae* is
25 not yet known. Since most micro-organisms for which the entire genome sequence is known (for example *E. coli*, *S. cerevisiae* and *B. subtilis*) have either *pdxA* and *pdxJ* homologs or *SOR* and *SNO* homologs, but not both, it appears that most organisms that are capable of synthesizing PLP have either the well characterized Type A Pathway (for example *E. coli*, *Salmonella typhimurium*, and many other genera), or a distinctly
30 different and incompletely characterized pathway, e.g., the Type B Pathway. Specifically, members of the genera *Cercospora*, *Neurospora*, *Aspergillus*, *Saccharomyces*, *Bacillus*, *Arabidopsis*, and many other genera, appear to have a Type B pathway, and are lacking genes involved in the Type A Pathway. The intermediate compounds in the Type B Pathway have not yet been elucidated, although the final
35 product must be PLP (as for the Type A Pathway) or PMP, since these are the active forms of vitamin B6 in all known organisms.

60368518-032902

Summary of the Invention

The present invention is based, at least in part, on the discovery of key enzyme-encoding genes of the B6 vitamer biosynthetic pathways in *Bacillus subtilis*. In particular, the invention is based, at least in part, on the discovery that the *yaaD* and *yaaE* genes of *B. subtilis* are required for B6 vitamer synthesis. Deletion of a portion of the *yaaD* and *yaaE* genes (which are adjacent in an operon, *e.g.*, the *yaaDE* operon) leads to PL auxotrophy. Overexpression of the *yaaDE* operon or the deregulation of the expression of the *yaaD* or *yaaE* genes leads to significantly increased production of B6 vitamers in, *e.g.*, *B. subtilis* strains. The *B. subtilis yaaDE* operon is required for pyridoxal phosphate (PLP) biosynthesis, an active form of vitamin B6 in all living organisms. The present invention describes that the expression of the *B. subtilis yaaDE* operon is a rate limiting step for production of compounds related to vitamin B6 in a wild type strain.

Accordingly, the present invention features methods of producing B6 vitamers, including, but not limited to, pyridoxine (or pyridoxol (PN)), pyridoxal (PL), pyridoxamine (PM), or the 5' phosphorylated derivatives of any of the three aforementioned compounds (PNP, PLP, and PMP), using organisms in which the B6 vitamer pathway has been manipulated such that B6 vitamers are produced. Such methods include culturing a microorganism that overexpresses at least one B6 vitamer biosynthetic enzyme (*e.g.*, at least one of the *yaaD* or *yaaE* gene products), under conditions such that the B6 vitamer is produced. The production methods of the present invention further can include recovering the B6 vitamer.

The instant invention also features genetically modified organisms (*i.e.*, organisms that contain one or more modifications or mutations in the genome) that are capable of producing significantly more of a B6 vitamer than an unmodified parent organism. In particular, this invention features micro-organisms (including, for example, but not limited to, bacteria, yeasts, fungi, and algae) or macro-organisms such as plants that, when genetically modified, produce an increased amount, *e.g.*, at least about 10-fold more of a B6 vitamer, than the unmodified parent organism. Specific examples are given herein in which *Bacillus subtilis* and *Escherichia coli* strains have been genetically modified such that they produce significant amounts of a B6 vitamer. Accordingly, the present invention features organisms that have been genetically modified to increase the activity of one or more enzymes that catalyze(s) a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism.

Yet another aspect of the invention features recombinant microorganisms which overexpress at least one *Bacillus* (*e.g.*, *B. subtilis*) B6 vitamer biosynthetic

60366618.032902

enzyme (e.g., at least one of the *yaaD* or *yaaE* gene products) are described. In one embodiment, the recombinant microorganism is Gram positive (e.g., microorganisms belonging to the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* or *Streptomyces*). In another embodiment, the recombinant microorganism is Gram
5 negative. Particularly preferred is a *Bacillus* recombinant microorganism (e.g., *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, *Bacillus pumilus*, *Bacillus halodurans*, and the like).

Recombinant vectors that contain genes encoding *Bacillus* B6 vitamers biosynthetic enzymes, e.g., *yaaD* or *yaaE* genes, are also described.
10

Other features and advantages of the invention will be apparent from the following detailed description and claims.

Brief Description of the Drawings

15 *Figure 1* depicts the chemical structures of vitamin B6 and related compounds.

Figure 2 depicts the biosynthetic pathway for PLP in *E. coli*.

Figure 3 depicts the standard curves generated by *Saccharomyces unarum* strain ATCC 9080 after feeding serial dilutions of PN, PL, and PM (as
20 described in Example 1).

Figure 4 is a schematic representation of the plasmid pDX1F.

Figure 5 is a schematic representation of the plasmid pDX11F.

Figure 6 is a schematic representation of the plasmid pDX14R.

Figure 7 is a schematic representation of the plasmid pDX17R.
25

Detailed Description of the Invention

The present invention is based, at least in part, on the identification of *Bacillus* (e.g., *B. subtilis*) genes that encode essential enzymes of the B6 vitamers biosynthetic pathway. In particular, the present invention features methods based on
30 manipulation of the B6 vitamers biosynthetic pathway in a microorganism such that certain desirable compounds are produced.

In particular, the invention is based, at least in part, on the discovery that the *yaaD* and *yaaE* genes of *B. subtilis* are required for B6 vitamers synthesis, including, but not limited to, pyridoxine (or pyridoxol (PN)), pyridoxal (PL), pyridoxamine (PM),
35 or the 5' phosphorylated derivatives of any of the three aforementioned compounds (PNP, PLP, and PMP). The *yaaD* and *yaaE* genes are adjacent on an operon, e.g., the *yaaDE* operon. The *yaaD* and *yaaE* genes encode the YaaD and Yaa E proteins,

respectively. Overexpression of the *yaaDE* operon with a strong constitutive promoter or the deregulation of the expression of the *yaaD* or *yaaE* gene(s) leads to significantly increased production of B6 vitamers. These quantities are significantly higher relative to the associated parent strains than those reported in previous studies, which have
5 employed mutant *E. coli* strains (Dempsey and Arcement (1971) *J. Bacteriol.* 107 (2): 580-582), or mutant *B. subtilis* strains (Pflug, W., and Lingens, F., (1978) Hoppe-Seyler's Z. Physiol. Chem. 359: 559-570).

Accordingly, the present invention features organisms that have been genetically modified to increase the activity of one or more enzymes that catalyze a step
10 in the biosynthesis of a B6 vitamer, such that B6 vitamer production from the modified organism is increased compared to B6 production in an unmodified parent organism. In one embodiment, B6 vitamer production is at least ten-fold higher than from the unmodified parent organism. In another embodiment, the organism is genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step
15 in the biosynthesis of a B6 vitamer, e.g., *yaaD* or *yaaE*. The organism may be, for example, *B. subtilis*.

The present invention also features methods of producing a B6 vitamer comprising culturing a microorganism that has been genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a
20 B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism, under conditions such that the B6 vitamer is produced. The B6 vitamer may then be subsequently recovered. Overproduction of the rate limiting enzyme for B6 vitamer production in any organism that is capable of producing B6 vitamers will lead to overproduction of B6 vitamers.

The terms "B6 vitamer" or "B6 vitamers," as used herein, shall refer to any compound or mixture of compounds that has any biological activity in any biological assay for vitamin B6. B6 vitamers include, but are not limited to, pyridoxine (also called pyridoxol or PN), pyridoxal (PL), pyridoxamine (PM), the 5'
25 phosphorylated derivatives of any of the three aforementioned compounds (PNP, PLP, and PMP), and any derivative or related compound that can be converted to the active forms (PLP or PMP) in a test organism. Thus, for example, the acetate esters or other esters of any of the available hydroxyl groups of any of the aforementioned six compounds, and which are likely to be hydrolyzed by specific or non-specific esterases, are included in B6 vitamers. Also, various salts, such as hydrochloride salts, of any of
30 the aforementioned compounds are included in B6 vitamers.

The term "B6 vitamer biosynthetic pathway" includes the biosynthetic pathway involving B6 vitamer biosynthetic enzymes (e.g., polypeptides encoded by

00368618-032900

biosynthetic enzyme-encoding genes), compounds (*e.g.*, precursors, substrates, intermediates or products), cofactors and the like utilized in the formation or synthesis of B6 vitamers. The term "B6 vitamer biosynthetic pathway" includes the biosynthetic pathway leading to the synthesis of B6 vitamers in a microorganism (*e.g.*, *in vivo*) as well as the biosynthetic pathway leading to the synthesis of B6 vitamers *in vitro*.

A "biological assay for a B6 vitamer" includes, for example, any assay that is capable of quantifying B6 vitamer activity by measuring growth of an organism that requires the feeding of a B6 vitamer (*i.e.*, a compound that the fed organism can convert into PLP or PMP) for growth. Samples to be assayed are diluted serially in an appropriate medium and fed to the appropriate organism. Standard curves are generated by serially diluting known amounts of PL, PN, or PM, and feeding these dilutions to the test organism. By comparing dilutions of the unknown samples to the standard curves, total B6 vitamer activity can be determined, for example as PL equivalents if PL was used to generate the standard curve.

Various aspects of the invention are described in further detail in the following subsections.

I. Genes Encoding Various B6 Vitamer Biosynthetic Enzymes

In one embodiment, the present invention features targeting or modifying various biosynthetic genes or enzymes of the B6 vitamer biosynthetic pathway. In particular, the invention features modifying various enzymatic activities associated with said pathways by modifying or altering the genes encoding said biosynthetic enzymes.

The term "gene", as used herein, includes a nucleic acid molecule (*e.g.*, a DNA molecule or segment thereof) that, in an organism, can be separated from another gene or other genes, by intergenic DNA (*i.e.*, intervening or spacer DNA which naturally flanks the gene and/or separates genes in the chromosomal DNA of the organism). Alternatively, a gene may slightly overlap another gene (*e.g.*, the 3' end of a first gene overlapping the 5' end of a second gene), said overlapping genes separated from other genes by intergenic DNA. A gene may direct synthesis of an enzyme or other protein molecule (*e.g.*, may comprise coding sequences, for example, a contiguous open reading frame (ORF) which encodes a protein) or may itself be functional in the organism. A gene in an organism, may be clustered in an operon, as defined herein, said operon being separated from other genes and/or operons by the intergenic DNA. An "isolated gene", as used herein, includes a gene which is essentially free of sequences which naturally flank the gene in the chromosomal DNA of the organism from which the gene is derived (*i.e.*, is free of adjacent coding sequences which encode a second or

60368618-032902

distinct protein, adjacent structural sequences or the like) and optionally includes 5' and 3' regulatory sequences, for example promoter sequences and/or terminator sequences. In one embodiment, an isolated gene includes predominantly coding sequences for a protein (e.g., sequences which encode *Bacillus* proteins). In another embodiment, an isolated gene includes coding sequences for a protein (e.g., for a *Bacillus* protein) and adjacent 5' and/or 3' regulatory sequences from the chromosomal DNA of the organism from which the gene is derived (e.g., adjacent 5' and/or 3' *Bacillus* regulatory sequences). Preferably, an isolated gene contains less than about 10 kb, 5 kb, 2 kb, 1 kb, 0.5 kb, 0.2 kb, 0.1 kb, 50 bp, 25 bp or 10 bp of nucleotide sequences that naturally flank the gene in the chromosomal DNA of the organism from which the gene is derived.

The term "operon" includes at least two adjacent genes or ORFs, optionally overlapping in sequence at either the 5' or 3' end of at least one gene or ORF. The term "operon" includes a coordinated unit of gene expression that contains a promoter and possibly a regulatory element associated with one or more adjacent genes or ORFs (e.g., structural genes encoding enzymes, for example, biosynthetic enzymes). Expression of the genes (e.g., structural genes) can be coordinately regulated, for example, by regulatory proteins binding to the regulatory element or by anti-termination of transcription. The genes of an operon (e.g., structural genes) can be transcribed to give a single mRNA that encodes all of the proteins.

A "gene having a mutation" or "mutant gene" as used herein, includes a gene having a nucleotide sequence which includes at least one alteration (e.g., substitution, insertion, deletion) such that the polypeptide or protein encoded by said mutant exhibits an activity that differs from the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. In one embodiment, a gene having a mutation or mutant gene encodes a polypeptide or protein having an increased activity as compared to the polypeptide or protein encoded by the wild-type gene, for example, when assayed under similar conditions (e.g., assayed in microorganisms cultured at the same temperature). As used herein, an "increased activity" or "increased enzymatic activity" is one that is at least 5% greater than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene, preferably at least 5-10% greater, more preferably at least 10-25% greater and even more preferably at least 25-50%, 50-75% or 75-100% greater than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. Ranges intermediate to the above-recited values, e.g., 75-85%, 85-90%, 90-95%, are also intended to be encompassed by the present invention. As used herein, an "increased activity" or "increased enzymatic activity" can also include an activity that is at least 1.25-fold greater than the activity of the polypeptide or protein encoded by the wild-type gene, preferably at least 1.5-fold

60368618-032902

greater, more preferably at least 2-fold greater and even more preferably at least 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or greater than the activity of the polypeptide or protein encoded by the wild-type gene.

In another embodiment, a gene having a mutation or mutant gene
5 encodes a polypeptide or protein having a reduced activity as compared to the polypeptide or protein encoded by the wild-type gene, for example, when assayed under similar conditions (*e.g.*, assayed in microorganisms cultured at the same temperature). A mutant gene also can encode no polypeptide or have a reduced level of production of the wild-type polypeptide. As used herein, a "reduced activity" or "reduced enzymatic
10 activity" is one that is at least 5% less than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene, preferably at least 5-10% less, more preferably at least 10-25% less and even more preferably at least 25-50%, 50-75% or 75-100% less than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene. Ranges intermediate to the above-recited values, *e.g.*, 75-85%,
15 85-90%, 90-95%, are also intended to be encompassed by the present invention. As used herein, a "reduced activity" or "reduced enzymatic activity" can also include an activity that has been deleted or "knocked out" (*e.g.*, approximately 100% less activity than that of the polypeptide or protein encoded by the wild-type nucleic acid molecule or gene).

20 Activity can be determined according to any well accepted assay for measuring activity of a particular protein of interest. Activity can be measured or assayed directly, for example, measuring an enzymatic or biological activity of a protein isolated or purified from a cell or microorganism. Alternatively, an activity can be measured or assayed within a cell or microorganism or in an extracellular medium. For
25 example, assaying for a mutant gene (*i.e.*, said mutant encoding a reduced enzymatic activity) can be accomplished by expressing the mutated gene in a microorganism, for example, a mutant microorganism in which the enzyme is temperature-sensitive, and assaying the mutant gene for the ability to complement a temperature sensitive (Ts) mutant for enzymatic activity. A mutant gene that encodes an "increased enzymatic
30 activity" can be one that complements the Ts mutant more effectively than, for example, a corresponding wild-type gene. A mutant gene that encodes a "reduced enzymatic activity" is one that complements the Ts mutant less effectively than, for example, a corresponding wild-type gene.

It will be appreciated by the skilled artisan that even a single substitution
35 in a nucleic acid or gene sequence (*e.g.*, a base substitution that encodes an amino acid change in the corresponding amino acid sequence) can dramatically affect the activity of an encoded polypeptide or protein as compared to the corresponding wild-type

2066220 0199909

polypeptide or protein. A mutant gene (e.g., encoding a mutant polypeptide or protein), as defined herein, is readily distinguishable from a nucleic acid or gene encoding a protein homologue in that a mutant gene encodes a protein or polypeptide having an altered activity, optionally observable as a different or distinct phenotype in a

5 microorganism expressing said mutant gene or producing said mutant protein or polypeptide (i.e., a mutant microorganism) as compared to a corresponding microorganism expressing the wild-type gene. By contrast, a protein homologue has an identical or substantially similar activity, optionally phenotypically indiscernible when produced in a microorganism, as compared to a corresponding microorganism

10 expressing the wild-type gene. Accordingly it is not, for example, the degree of sequence identity between nucleic acid molecules, genes, protein or polypeptides that serves to distinguish between homologues and mutants, rather it is the activity of the encoded protein or polypeptide that distinguishes between homologues and mutants: homologues having, for example, low (e.g., 30-50% sequence identity) sequence

15 identity yet having substantially equivalent functional activities, and mutants, for example sharing 99% sequence identity yet having dramatically different or altered functional activities.

In a preferred embodiment, the genes of the present invention are derived from *Bacillus*. The term "derived from *Bacillus*" or "*Bacillus*-derived" includes a gene

20 which is naturally found in microorganisms of the genus *Bacillus*. In another preferred embodiment, the genes of the present invention are derived from a microorganism selected from the group consisting of *Bacillus subtilis*, *Bacillus lentimorbus*, *Bacillus lentus*, *Bacillus firmus*, *Bacillus pantothenicus*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus*

25 *megaterium*, *Bacillus pumilus*, *Bacillus thuringiensis*, *Bacillus halodurans*, and other Group 1 *Bacillus* species, for example, as characterized by 16S rRNA type. In another preferred embodiment, the gene is derived from *Bacillus brevis* or *Bacillus stearothermophilus*. In another preferred embodiment, the genes of the present invention are derived from a microorganism selected from the group consisting of

30 *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, and *Bacillus pumilus*. In a particularly preferred embodiment, the gene is derived from *Bacillus subtilis* (e.g., is *Bacillus subtilis*-derived). The term "derived from *Bacillus subtilis*" or "*Bacillus subtilis*-derived" includes a gene which is naturally found in the microorganism *Bacillus subtilis*. Included within the scope of the present invention are

35 *Bacillus*-derived genes (e.g., *B. subtilis*-derived genes), for example, *Bacillus* or *B. subtilis yaaD* or *yaaE* genes.

50366618.032902

II. Recombinant Nucleic Acid Molecules and Vectors

5 The present invention further features recombinant nucleic acid molecules (*e.g.*, recombinant DNA molecules) that include genes described herein (*e.g.*, isolated genes), preferably *Bacillus* genes, more preferably *Bacillus subtilis* genes, even
10 more preferably *Bacillus subtilis* B6 vitamer biosynthetic genes. The term "recombinant nucleic acid molecule" includes an isolated nucleic acid molecule (*e.g.*, a DNA molecule) that has been altered, modified or engineered such that it differs in nucleotide sequence from the native or natural nucleic acid molecule from which the recombinant
15 nucleic acid molecule was derived (*e.g.*, by addition, deletion or substitution of one or more nucleotides). Preferably, a recombinant nucleic acid molecule (*e.g.*, a recombinant DNA molecule) includes an isolated gene of the present invention operably linked to regulatory sequences. The phrase "operably linked to regulatory sequence(s)" means that the nucleotide sequence of the gene of interest is linked to the regulatory
20 sequence(s) in a manner which allows for expression (*e.g.*, enhanced, increased, constitutive, basal, attenuated, decreased or repressed expression) of the gene, preferably expression of a gene product encoded by the gene (*e.g.*, when the recombinant nucleic acid molecule is included in a recombinant vector, as defined herein, and is introduced into a microorganism). A "recombinant organism" is any organism that contains a recombinant nucleic acid molecule.

20 The term "regulatory sequence" includes nucleic acid sequences that affect (*e.g.*, modulate or regulate) expression of other nucleic acid sequences (*i.e.*, genes). In one embodiment, a regulatory sequence is included in a recombinant nucleic acid molecule in a similar or identical position and/or orientation relative to a particular gene of interest as is observed for the regulatory sequence and gene of interest as it
25 appears in nature, *e.g.*, in a native position and/or orientation. For example, a gene of interest can be included in a recombinant nucleic acid molecule operably linked to a regulatory sequence which accompanies or is adjacent to the gene of interest in the natural organism (*e.g.*, operably linked to "native" regulatory sequences (*e.g.*, to the "native" promoter). Alternatively, a gene of interest can be included in a recombinant
30 nucleic acid molecule operably linked to a regulatory sequence which accompanies or is adjacent to another (*e.g.*, a different) gene in the natural organism. Alternatively, a gene of interest can be included in a recombinant nucleic acid molecule operably linked to a regulatory sequence from another organism. For example, regulatory sequences from other microbes (*e.g.*, other bacterial regulatory sequences, bacteriophage regulatory
35 sequences and the like) can be operably linked to a particular gene of interest.

In one embodiment, a regulatory sequence is a non-native or non-naturally-occurring sequence (*e.g.*, a sequence which has been modified, mutated,

substituted, derivatized, deleted including sequences which are chemically synthesized). Preferred regulatory sequences include promoters, enhancers, termination signals, anti-termination signals, ribosome binding sites and other expression control elements (e.g., sequences to which repressors or inducers bind and/or binding sites for transcriptional and/or translational regulatory proteins, for example, in the transcribed mRNA). Such regulatory sequences are described, for example, in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989. Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in a microorganism (e.g., constitutive promoters and strong constitutive promoters), those which direct inducible expression of a nucleotide sequence in a microorganism (e.g., inducible promoters, for example, xylose inducible promoters) and those which attenuate or repress expression of a nucleotide sequence in a microorganism (e.g., attenuation signals or repressor sequences). It is also within the scope of the present invention to regulate expression of a gene of interest by removing or deleting regulatory sequences. For example, sequences involved in the negative regulation of transcription can be removed such that expression of a gene of interest is enhanced.

In one embodiment, a recombinant nucleic acid molecule of the present invention includes a nucleic acid sequence or gene that encodes at least one bacterial gene product (e.g., a B6 vitamer biosynthetic enzyme, e.g., the gene product of *yaaD* and/or *yaaE*) operably linked to a promoter or promoter sequence. Preferred promoters of the present invention include *Bacillus* promoters and/or bacteriophage promoters (e.g., bacteriophage which infect *Bacillus*). In one embodiment, a promoter is a *Bacillus* promoter, preferably a strong *Bacillus* promoter (e.g., a promoter associated with a biochemical housekeeping gene in *Bacillus* or a promoter associated with a glycolytic pathway gene in *Bacillus*). In another embodiment, a promoter is a bacteriophage promoter. In a preferred embodiment, the promoter is from the bacteriophage SP01. In a particularly preferred embodiment, a promoter is selected from the group consisting of *P₁₅*, *P₂₆*, or *P_{veg}* having for example, the following respective sequences:

30 GCTATTGACGACAGCTATGGTTCACTGTCCACCAACCAAACTGTGCTCAGT
ACCGCCAATATTTCTCCCTTGAGGGGTACAAAGAGGTGTCCCTAGAAGAGAT
CCACGCTGTGTAAAAATTTACAAAAAGGTATTGACTTTCCCTACAGGGTGT
GTAATAATTTAATTACAGGCGGGGCAACCCCGCCTGT (SEQ ID NO:9),
GCCTACCTAGCTTCCAAGAAAGATATCCTAACAGCACAAGAGCGGAAAGAT
35 GTTTTGTCTACATCCAGAACAACCTCTGCTAAAATTCCTGAAAAATTTTGC
AAAAAGTTGTTGACTTTATCTACAAGGTGTGGTATAATAATCTTAACAACAG
CAGGACGC (SEQ ID NO:10); and

60368618.0322902

GAGGAATCATAGAATTTTGTCAAAATAATTTTATTGACAACGCTTTATTAAC
 GTTGATATAATTTAAATTTTATTTGACAAAAATGGGCTCGTGTGTACAATA
 AATGTAGTGAGGTGGATGCAATG (SEQ ID NO:11). Additional preferred

promoters include *tef* (the translational elongation factor (TEF) promoter) and *pyc* (the
 5 pyruvate carboxylase (PYC) promoter), which promote high level expression in *Bacillus*
 (*e.g.*, *Bacillus subtilis*). Additional preferred promoters, for example, for use in Gram
 positive microorganisms include, but are not limited to, *amy* and SPO2 promoters.
 Additional preferred promoters, for example, for use in Gram negative microorganisms
 include, but are not limited to, *tac*, *trp*, *tet*, *trp-tet*, *lpp*, *lac*, *lpp-lac*, *lacIQ*, T7, T5, T3,
 10 *gal*, *trc*, *ara*, SP6, λ -PR or λ -PL.

In another embodiment, a recombinant nucleic acid molecule of the
 present invention includes a terminator sequence or terminator sequences (*e.g.*,
 transcription terminator sequences). The term "terminator sequences" includes
 regulatory sequences that serve to terminate transcription of mRNA. Terminator
 15 sequences (or tandem transcription terminators) can further serve to stabilize mRNA
 (*e.g.*, by adding structure to mRNA), for example, against nucleases.

In yet another embodiment, a recombinant nucleic acid molecule of the
 present invention includes sequences which allow for detection of the vector containing
 said sequences (*i.e.*, detectable and/or selectable markers), for example, genes that
 20 encode antibiotic resistance or sequences that overcome auxotrophic mutations, for
 example, *trpC*, fluorescent markers, drug markers, and/or colorimetric markers (*e.g.*,
lacZ/ β -galactosidase). In yet another embodiment, a recombinant nucleic acid molecule
 of the present invention includes an artificial ribosome binding site (RBS) or a sequence
 that becomes transcribed into an artificial RBS. The term "artificial ribosome binding
 25 site (RBS)" includes a site within an mRNA molecule (*e.g.*, coded within DNA) to
 which a ribosome binds (*e.g.*, to initiate translation) which differs from a native RBS
 (*e.g.*, a RBS found in a naturally-occurring gene) by at least one nucleotide. Preferred
 artificial RBSs include about 5-6, 7-8, 9-10, 11-12, 13-14, 15-16, 17-18, 19-20, 21-22,
 23-24, 25-26, 27-28, 29-30 or more nucleotides of which about 1-2, 3-4, 5-6, 7-8, 9-10,
 30 11-12, 13-15 or more differ from the native RBS (*e.g.*, the native RBS of a gene of
 interest, for example, the native *yaaD* RBS

GAAATCATATAACTATACCTTGATTAGGGGGACCAAGAAATG
 (SEQ ID NO:12) or the native *yaaE* RBS
 CAAGAACGCGGCTGGTAAGAACATAGGAGCGCTGCTGACATG (SEQ ID
 35 NO:13)).

Preferably, nucleotides that differ are substituted such that they are
 identical to one or more nucleotides of an ideal RBS when optimally aligned for

206220" BT 999999

comparisons. Artificial RBSs can be used to replace the naturally-occurring or native RBSs associated with a particular gene. Artificial RBSs preferably increase translation of a particular gene. Preferred artificial RBSs (e.g., RBSs for increasing the translation of *yaaE*, for example, of *B. subtilis*) are set forth in Table 1, below.

Table 1: Preferred Ribosome Binding Sites

	10	20	
10			SEQ ID NO:
	Native_yaaD ---GAAATCATATAACTATACCTTGATTAGGGGGACC-AAGAAATG		12
	Native_yaaE CAAGAACGCGGCTGGTAAGAACAT---AGGAGCGCTGCTGACATG		13
	IDEAL_RBS -----TCTAGAAAGG---AGGTG-----A-----		14
	RBS1 -----TCTAGAAAGG---AGGAG-----AAAACATG		15
15	RBS2 -----TCTAGAGG---AGGAG-----AAAACATG		16
	RBS101 -----TAAGAACAA---AGGAGGAGAGCTGACATG		17
	RBS103 -----TAAGAAGAA---AGGAGGTGAGCTGACATG		18
	RBS102 -----TAAGAACAG---AGGAGGAGAGCTGACATG		19

The present invention further features vectors (e.g., recombinant vectors) that include nucleic acid molecules (e.g., genes or recombinant nucleic acid molecules comprising said genes) as described herein. The term "recombinant vector" includes a vector (e.g., plasmid, phage, phasmid, virus, cosmid or other purified nucleic acid vector) that has been altered, modified or engineered such that it contains greater, fewer or different nucleic acid sequences than those included in the native or natural nucleic acid molecule from which the recombinant vector was derived. Preferably, the recombinant vector includes a biosynthetic enzyme-encoding gene or recombinant nucleic acid molecule including said gene, operably linked to regulatory sequences, for example, promoter sequences, terminator sequences and/or artificial ribosome binding sites (RBSs), as defined herein. In another embodiment, a recombinant vector of the present invention includes sequences that enhance replication in bacteria (e.g., replication-enhancing sequences). In one embodiment, replication-enhancing sequences are derived from *E. coli*. In another embodiment, replication-enhancing sequences are derived from pBR322. In another embodiment, replication-enhancing sequences are derived from pSC101.

In yet another embodiment, a recombinant vector of the present invention includes antibiotic resistance sequences. The term "antibiotic resistance sequences" includes sequences which promote or confer resistance to antibiotics on the host organism (e.g., *Bacillus*). In one embodiment, the antibiotic resistance sequences are selected from the group consisting of *cat* (chloramphenicol resistance) sequences, *tet* (tetracycline resistance) sequences, *erm* (erythromycin resistance) sequences, *neo*

(neomycin resistance) sequences, *kan* (kanamycin resistance) and *spec* (spectinomycin resistance) sequences. Recombinant vectors of the present invention can further include homologous recombination sequences (e.g., sequences designed to allow recombination of the gene of interest into the chromosome of the host organism). For example, *bpr*, *vpr*, and/or *amyE* sequences can be used as homology targets for recombination into the host chromosome. It will further be appreciated by one of skill in the art that the design of a vector can be tailored depending on such factors as the choice of microorganism to be genetically engineered, the level of expression of gene product desired and the like.

III. Recombinant Microorganisms

The present invention further features microorganisms, i.e., recombinant microorganisms, that include vectors or genes (e.g., wild-type and/or mutated genes) as described herein. As used herein, the term "recombinant microorganism" includes a microorganism (e.g., bacteria, yeast cell, fungal cell, etc.) that has been genetically altered, modified or engineered (e.g., genetically engineered) such that it exhibits an altered, modified or different genotype and/or phenotype (e.g., when the genetic modification affects coding nucleic acid sequences of the microorganism) as compared to the naturally-occurring microorganism from which it was derived.

In one embodiment, a recombinant microorganism of the present invention is a Gram positive organism (e.g., a microorganism which retains basic dye, for example, crystal violet, due to the presence of a Gram-positive wall surrounding the microorganism). In a preferred embodiment, the recombinant microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*. In a more preferred embodiment, the recombinant microorganism is of the genus *Bacillus*. In another preferred embodiment, the recombinant microorganism is selected from the group consisting of *Bacillus subtilis*, *Bacillus lentimorbus*, *Bacillus lentus*, *Bacillus firmus*, *Bacillus pantothenicus*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus thuringiensis*, *Bacillus halodurans*, and other Group 1 *Bacillus* species, for example, as characterized by 16S rRNA type. In another preferred embodiment, the recombinant microorganism is *Bacillus brevis* or *Bacillus stearothermophilus*. In another preferred embodiment, the recombinant microorganism is selected from the group consisting of *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus subtilis*, and *Bacillus pumilus*.

In another embodiment, the recombinant microorganism is a Gram negative (excludes basic dye) organism. In a preferred embodiment, the recombinant

206220 8199909

microorganism is a microorganism belonging to a genus selected from the group consisting of *Salmonella*, *Escherichia*, *Klebsiella*, *Serratia*, and *Proteus*. In a more preferred embodiment, the recombinant microorganism is of the genus *Escherichia*. In an even more preferred embodiment, the recombinant microorganism is *Escherichia coli*. In another embodiment, the recombinant microorganism is *Saccharomyces* (e.g., *S. cerevisiae*).

5 A preferred "recombinant" microorganism of the present invention is a microorganism having a deregulated B6 vitamer biosynthesis pathway or enzyme. The term "deregulated" or "deregulation" includes the alteration or modification of at least
10 one gene in a microorganism that encodes an enzyme in a biosynthetic pathway, such that the level or activity of the biosynthetic enzyme in the microorganism is altered or modified. Preferably, at least one gene that encodes an enzyme in a biosynthetic pathway is altered or modified such that the gene product is enhanced or increased. The phrase "deregulated pathway" can also include a biosynthetic pathway in which more
15 than one gene that encodes an enzyme in a biosynthetic pathway is altered or modified such that the level or activity of more than one biosynthetic enzyme is altered or modified. The ability to "deregulate" a pathway (e.g., to simultaneously deregulate more than one gene in a given biosynthetic pathway) in a microorganism in some cases arises from the particular phenomenon of microorganisms in which more than one
20 enzyme (e.g., two or three biosynthetic enzymes) are encoded by genes occurring adjacent to one another on a contiguous piece of genetic material termed an "operon" (defined herein). Due to the coordinated regulation of genes included in an operon, alteration or modification of the single promoter and/or regulatory element can result in alteration or modification of the expression of more than one gene product encoded by
25 the operon. Alteration or modification of the regulatory element can include, but is not limited to removing the endogenous promoter and/or regulatory element(s), adding strong promoters, inducible promoters or multiple promoters or removing regulatory sequences such that expression of the gene products is modified, modifying the chromosomal location of the operon, altering nucleic acid sequences adjacent to the
30 operon or within the operon such as a ribosome binding site, increasing the copy number of the operon, modifying proteins (e.g., regulatory proteins, suppressors, enhancers, transcriptional activators and the like) involved in transcription of the operon and/or translation of the gene products of the operon, or any other conventional means of deregulating expression of genes routine in the art (including but not limited to use of
35 antisense nucleic acid molecules, for example, to block expression of repressor proteins). Deregulation can also involve altering the coding region of one or more genes

60368510.032902

to yield, for example, an enzyme that is feedback resistant or has a higher or lower specific activity.

In another preferred embodiment, a recombinant microorganism is designed or engineered such that at least one B6 vitamer biosynthetic enzyme, is overexpressed. The term "overexpressed" or "overexpression" includes expression of a gene product (e.g., a biosynthetic enzyme) at a level greater than that expressed prior to manipulation of the microorganism or in a comparable microorganism which has not been manipulated. In one embodiment, the microorganism can be genetically designed or engineered to overexpress a level of gene product greater than that expressed in a comparable microorganism which has not been engineered.

Genetic engineering can include, but is not limited to, altering or modifying regulatory sequences or sites associated with expression of a particular gene (e.g., by adding strong promoters, inducible promoters or multiple promoters or by removing regulatory sequences such that expression is constitutive), modifying the chromosomal location of a particular gene, altering nucleic acid sequences adjacent to a particular gene such as a ribosome binding site, increasing the copy number of a particular gene, modifying proteins (e.g., regulatory proteins, suppressors, enhancers, transcriptional activators and the like) involved in transcription of a particular gene and/or translation of a particular gene product, or any other conventional means of deregulating expression of a particular gene routine in the art (including but not limited to use of antisense nucleic acid molecules, for example, to block expression of repressor proteins). Genetic engineering can also include deletion of a gene, for example, to block a pathway or to remove a repressor. In embodiments featuring microorganisms having deleted genes, the skilled artisan will appreciate that at least low levels of certain compounds may be required to be present in or added to the culture medium in order that the viability of the microorganism is not compromised. Often, such low levels are present in complex culture media as routinely formulated. Moreover, in processes featuring culturing microorganisms having deleted genes cultured under conditions such that commercially or industrially attractive quantities of product are produced, it may be necessary to supplement culture media with slightly increased levels of certain compounds.

In another embodiment, the microorganism can be physically or environmentally manipulated to overexpress a level of gene product greater than that expressed prior to manipulation of the microorganism or in a comparable microorganism which has not been manipulated. For example, a microorganism can be treated with or cultured in the presence of an agent known or suspected to increase transcription of a particular gene and/or translation of a particular gene product such that transcription

50366618 032902

and/or translation are enhanced or increased. Alternatively, a microorganism can be cultured at a temperature selected to increase transcription of a particular gene and/or translation of a particular gene product such that transcription and/or translation are enhanced or increased.

5

IV: Culturing and Fermenting Recombinant Microorganisms

The term "culturing" includes maintaining and/or growing a living microorganism of the present invention (e.g., maintaining and/or growing a culture or strain). In one embodiment, a microorganism of the invention is cultured in liquid media. In another embodiment, a microorganism of the invention is cultured in solid media or semi-solid media. In a preferred embodiment, a microorganism of the invention is cultured in media (e.g., a sterile, liquid media) comprising nutrients essential or beneficial to the maintenance and/or growth of the microorganism (e.g., carbon sources or carbon substrate, for example carbohydrate, hydrocarbons, oils, fats, fatty acids, organic acids, and alcohols; nitrogen sources, for example, peptone, yeast extracts, meat extracts, malt extracts, soy flour, urea, ammonium sulfate, ammonium chloride, ammonium nitrate and ammonium phosphate; phosphorus sources, for example, phosphoric acid, sodium and potassium salts thereof; trace elements, for example, magnesium, iron, manganese, calcium, copper, zinc, boron, molybdenum, and/or cobalt salts; as well as growth factors such as amino acids, vitamins, and the like).

Preferably, microorganisms of the present invention are cultured under controlled pH. The term "controlled pH" includes any pH which results in production of the desired product. In one embodiment microorganisms are cultured at a pH of about 7. In another embodiment, microorganisms are cultured at a pH of between 6.0 and 8.5. The desired pH may be maintained by any number of methods known to those skilled in the art.

Also preferably, microorganisms of the present invention are cultured under controlled aeration. The term "controlled aeration" includes sufficient aeration (e.g., oxygen) to result in production of the desired product. In one embodiment, aeration is controlled by regulating oxygen levels in the culture, for example, by regulating the amount of oxygen dissolved in culture media. Preferably, aeration of the culture is controlled by agitating the culture. Agitation may be provided by a propeller or similar mechanical agitation equipment, by revolving or shaking the culture vessel (e.g., tube or flask) or by various pumping equipment. Aeration may be further controlled by the passage of sterile air or oxygen through the medium (e.g., through the

fermentation mixture). Also preferably, microorganisms of the present invention are cultured without excess foaming (*e.g.*, *via* addition of antifoaming agents).

Moreover, microorganisms of the present invention can be cultured under controlled temperatures. The term "controlled temperature" includes any temperature which results in production of the desired product (*e.g.*, a B6 vitamer). In one embodiment, controlled temperatures include temperatures between 15°C and 95°C. In another embodiment, controlled temperatures include temperatures between 15°C and 70°C. Preferred temperatures are between 20°C and 55°C, more preferably between 30°C and 50°C.

Microorganisms can be cultured (*e.g.*, maintained and/or grown) in liquid media and preferably are cultured, either continuously or intermittently, by conventional culturing methods such as standing culture, test tube culture, shaking culture (*e.g.*, rotary shaking culture, shake flask culture, etc.), aeration spinner culture, or fermentation. In a preferred embodiment, the microorganisms are cultured in shake flasks. In a more preferred embodiment, the microorganisms are cultured in a fermentor (*e.g.*, a fermentation process). Fermentation processes of the present invention include, but are not limited to, batch, fed-batch and continuous processes or methods of fermentation. The phrase "batch process" or "batch fermentation" refers to a closed system in which the composition of media, nutrients, supplemental additives and the like is set at the beginning of the fermentation and not subject to alteration during the fermentation, however, attempts may be made to control such factors as pH and oxygen concentration to prevent excess media acidification and/or microorganism death. The phrase "fed-batch process" or "fed-batch" fermentation refers to a batch fermentation with the exception that one or more substrates or supplements are added (*e.g.*, added in increments or continuously) as the fermentation progresses. The phrase "continuous process" or "continuous fermentation" refers to a system in which a defined fermentation media is added continuously to a fermentor and an equal amount of used or "conditioned" media is simultaneously removed, preferably for recovery of the desired product (*e.g.*, a B6 vitamer). A variety of such processes have been developed and are well-known in the art.

The phrase "culturing under conditions such that a desired compound is produced" includes maintaining and/or growing microorganisms under conditions (*e.g.*, temperature, pressure, pH, duration, etc.) appropriate or sufficient to obtain production of the desired compound or to obtain desired yields of the particular compound being produced. For example, culturing is continued for a time sufficient to produce the desired amount of a compound (*e.g.*, a B6 vitamer). Preferably, culturing is continued for a time sufficient to substantially reach suitable production of the compound (*e.g.*, a

60368618-032902

time sufficient to reach a suitable concentration of a B6 vitamer). In one embodiment, culturing is continued for about 12 to 24 hours. In another embodiment, culturing is continued for about 24 to 36 hours, 36 to 48 hours, 48 to 72 hours, 72 to 96 hours, 96 to 120 hours, 120 to 144 hours, or greater than 144 hours. The methodology of the present invention can further include a step of recovering a desired compound (e.g., a B6 vitamer). The term "recovering" a desired compound includes extracting, harvesting, isolating or purifying the compound from culture media. Recovering the compound can be performed according to any conventional isolation or purification methodology known in the art including, but not limited to, treatment with a conventional resin (e.g., anion or cation exchange resin, non-ionic adsorption resin, etc.), treatment with a conventional adsorbent (e.g., activated charcoal, silicic acid, silica gel, cellulose, alumina, etc.), alteration of pH, solvent extraction (e.g., with a conventional solvent such as an alcohol, ethyl acetate, hexane and the like), dialysis, filtration, concentration, crystallization, recrystallization, pH adjustment, lyophilization and the like. For example, a compound can be recovered from culture media by first removing the microorganisms from the culture. The resulting solutions are then passed through or over a cation exchange resin to remove cations and/or through or over an anion exchange resin to purify or concentrate the desired product. The resulting compound can subsequently be converted to a salt (e.g., a chloride or sulfate salt) by ion exchange.

Preferably, a desired compound of the present invention is "extracted," "isolated" or "purified" such that the resulting preparation is substantially free of other media components (e.g., free of media components and/or fermentation byproducts). The language "substantially free of other media components" includes preparations of the desired compound in which the compound is separated from media components or fermentation byproducts of the culture from which it is produced. In one embodiment, the preparation has greater than about 80% (by dry weight) of the desired compound (e.g., less than about 20% of other media components or fermentation byproducts), more preferably greater than about 90% of the desired compound (e.g., less than about 10% of other media components or fermentation byproducts), still more preferably greater than about 95% of the desired compound (e.g., less than about 5% of other media components or fermentation byproducts), and most preferably greater than about 98-99% desired compound (e.g., less than about 1-2% other media components or fermentation byproducts). When the desired compound has been derivatized to a salt, the compound is preferably further free of chemical contaminants associated with the formation of the salt. When the desired compound has been derivatized to an alcohol, the compound is preferably further free of chemical contaminants associated with the formation of the alcohol.

50358618.032902

In an alternative embodiment, the desired compound is not purified from the microorganism, for example, when the microorganism is biologically non-hazardous (*e.g.*, safe). For example, the entire culture (or culture supernatant) can be used as a source of product (*e.g.*, crude product). In one embodiment, the culture (or culture supernatant) is used without modification. In another embodiment, the culture (or culture supernatant) is concentrated. In yet another embodiment, the culture (or culture supernatant) is dried or lyophilized.

Preferably, a production method of the present invention results in production of the desired compound, *e.g.*, a B6 vitamer, at a significantly high yield. The phrase "significantly high yield" includes a level of production or yield which is sufficiently elevated or above what is usual for comparable production methods, for example, which is elevated to a level sufficient for commercial production of the desired product (*e.g.*, production of the product at a commercially feasible cost). In one embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (*e.g.*, a B6 vitamer) is produced at a level greater than 5 mg/L. In another embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (*e.g.*, a B6 vitamer) is produced at a level greater than 10 mg/L. In another embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (*e.g.*, a B6 vitamer) is produced at a level greater than 50 mg/L. In yet another embodiment, the invention features a production method that includes culturing a recombinant microorganism under conditions such that the desired product (*e.g.*, a B6 vitamer) is produced at a level greater than 150 mg/L.

Depending on the biosynthetic enzyme or combination of biosynthetic enzymes manipulated, it may be desirable or necessary to provide (*e.g.*, feed) microorganisms of the present invention at least one biosynthetic precursor such that the desired compound or compounds are produced. The term "biosynthetic precursor" or "precursor" includes an agent or compound which, when provided to, brought into contact with, or included in the culture medium of a microorganism, serves to enhance or increase biosynthesis of the desired product. In one embodiment, the biosynthetic precursor or precursor is glutamine. In another embodiment, the biosynthetic precursor or precursor is ribose. The amount of glutamine or ribose added is preferably an amount that results in a concentration in the culture medium sufficient to enhance productivity of the microorganism (*e.g.*, a concentration sufficient to enhance production of a B6 vitamer). The term "excess ribose or glutamine" includes ribose or glutamine levels increased or higher than those routinely utilized for culturing the microorganism in

60368618.032902

question. For example, culturing the *Bacillus* microorganisms described in the instant Examples is routinely done in the presence of about 0-5 g/L ribose or glutamine.

Accordingly, excess ribose or glutamine levels can include levels of about 5-10 g/L or more preferably about 5-20 g/L ribose or glutamine. Biosynthetic precursors of the

5 present invention can be added in the form of a concentrated solution or suspension (e.g., in a suitable solvent such as water or buffer) or in the form of a solid (e.g., in the form of a powder). Moreover, biosynthetic precursors of the present invention can be added as a single aliquot, continuously or intermittently over a given period of time.

10

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents and published patent applications cited throughout this application are incorporated herein by reference.

15

60368518.032902

EXAMPLES

EXAMPLE 1: Biological assay for B6 vitamers using *Saccharomyces uvarum*.

Quantitation of B6 vitamers in supernatants of cultures of micro-organisms or extracts of organisms that have been genetically modified to increase production of B6 vitamers is conveniently done using *Saccharomyces uvarum* (formerly and still often named *S. carlsbergensis*) strain ATCC 9080 as the indicator strain or test organism. The method is essentially that described in the Difco Manual (1984, Difco Laboratories, Detroit, MI, 10th Edition, pp. 1104-1106), with the modification that 50 mg/liter of streptomycin sulfate is added to the liquid growth medium for the test organism. However, any other appropriate indicator organism may be used, together with a medium that is appropriate for that organism that is free of B6 vitamers. For example, an *E. coli* *padB* mutant can be used in a standard minimal medium that is well known in the art, such as M9 glucose minimal medium (Miller, J., (1972) Experiments in Molecular Genetics, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY).

When using *S. uvarum* strain ATCC 9080 as the indicator strain, Bacto Pyridoxine Y Medium (Difco Laboratories, available through VWR Scientific, Inc.), supplemented with 50 mg/liter streptomycin sulfate, is used for the serial dilutions, and PN, PL, or PM is used to generate the standard curve. The responses to these three standard compounds are almost identical to each other with *S. uvarum* strain ATCC 9080 (Figure 3).

EXAMPLE 2: Deletion of a portion of the *yaaDE* operon in *B. subtilis*.

The *SOR* and *SNO* genes of *Cercospora nicotianae* were originally identified by mutations that lead to hypersensitivity to singlet oxygen-generating reagents (Ehrenschaft, M., et al. (1999) *Proc. Natl. Acad. Sci. USA* 96: 9347-9378). Mutations in either of these genes also lead to PL auxotrophy. The protein sequences obtained from translation of the *SOR* and *SNO* open reading frames were used as homology probes to search through the *B. subtilis* genome sequence using the BLAST homology search program of the Subtilist website. The *SOR* protein was significantly homologous to the YaaD protein, and the *SNO* protein was significantly homologous to the YaaE protein. Moreover, the genes encoding the YaaD and YaaE proteins (namely *yaaD* and *yaaE*) occur adjacent to each other on the *B. subtilis* chromosome as a two gene operon.

General methods for growth, storage, transformation, and molecular biology of *B. subtilis* strains are given in Harwood, C., and Cutting, S. (1990), *Molecular Biological Methods for Bacillus*, John Wiley and Sons, New York, NY, hereby

incorporated in its entirety by reference. The *yaaDE* operon DNA sequence was amplified using the Polymerase Chain Reaction (PCR) with Pfu Turbo DNA polymerase (Stratagene, Inc., used according to the manufacturer's instructions). The DNA primers used were RY395 (SEQ ID NO:1) and RY396 (SEQ ID NO:2). RY395, the upstream
5 primer, introduces an *XbaI* site and artificial ribosome binding site. RY396, the downstream primer, introduces a *BamHI* site. The template DNA was chromosomal DNA isolated from wild type *B. subtilis* strain PY79. The blunt ended PCR product was ligated into the *EcoRV* site of pGEM5Zf(+) (Promega, Inc.) to give plasmid pAN368. Next, a gram positive chloramphenicol resistance gene on a blunt DNA fragment was
10 ligated into pAN368 that had been cut with *HpaI*, to give plasmid pDX1F (SEQ ID NO:5, Figure 4). pDX1F therefore is deleted for a portion of *yaaD* and a portion of *yaaE*. pDX1F was used to transform wild type *B. subtilis* strain PY79 to 5 mg/liter chloramphenicol resistance, and a double crossover event was confirmed using PCR and the same primers used to clone *yaaDE*. The resulting strain was named PX1.

15 PX1 was able to grow on Spizizen's minimal medium with trace elements (SMM) (Harwood, C., and Cutting, S. (1990) Molecular Biological Methods for *Bacillus*, John Wiley and Sons, New York, NY, pp. 548-549) supplemented with 2 μ M pyridoxal HCl (Sigma-Aldrich Chemical Co.), but it did not grow without the supplement. Thus it was established that at least one of *yaaD* or *yaaE* is required for
20 PLP synthesis in *B. subtilis*.

EXAMPLE 3: Deletion of *yhaF* in *B. subtilis*.

The protein sequence of the *E. coli pdxF* gene was used as a probe to search the *B. subtilis* genome as described in Example 1. The only significant homolog
25 was *yhaF*. In a fashion similar to that of Example 1, the *yhaF* was cloned and deleted from the chromosome of PY79 using plasmid pDX11F (SEQ ID NO:6, Figure 5), to give strain PX11. The PCR primers used to clone *yhaF* were RY407 (SEQ ID NO:3) and RY408 (SEQ ID NO:4). The restriction sites used for insertion of the antibiotic resistance gene were the *PshAI* and *EheI* sites in the *yhaF* coding region. PX11 is a
30 serine auxotroph, but not a PL auxotroph. By comparison to *E. coli*, it appears that *yhaF* functions in serine synthesis and probably encodes the equivalent of *SerC*, but that the YhaF protein is not required for PLP synthesis in *B. subtilis*. Therefore, it is established that sequence homology does not necessarily imply functional homology.

35 **EXAMPLE 4: Overexpression of the *yaaDE* operon in *B. subtilis*.**

The *XbaI* to *BamHI* fragment from pAN368 that contains the *yaaDE* operon and artificial ribosome binding site was inserted into either of two expression

60366618, 0329012

vectors, to yield plasmids pDX14R (SEQ ID NO:7) and pDX17R (SEQ ID NO:8), respectively. In pDX14R and pDX17R, the *yaaDE* operon is expressed from the strong constitutive *B. subtilis* phage SP01 promoters, P_{26} and P_{15} , respectively (see Figures 6 and 7).

5 pDX14R and pDX17R were each transformed into wild type *B. subtilis* strain PY79, selecting for chloramphenicol resistance. The plasmids integrate into the chromosome at the *yaaDE* locus by single crossover. The resulting strains were named PX14 and PX17, respectively.

10 PX14 and PX17 were grown for 48 hours at 37°C in 5 ml test tube cultures in a roller drum at about 100 rotations per minute. The culture medium was SVY (20 g Difco Veal Infusion Broth, 5 g Difco Yeast Extract, 2 g ammonium sulfate, 5 g sodium glutamate, and 30 g glucose per liter, buffered with 200 mM potassium phosphate, pH 7.0). Cells were removed by centrifugation followed by sterile filtration (Millipore 0.45 micron), and the supernatant solutions were assayed for PL equivalents using the biological assay described in Example 1. The parent strain, PY79 was grown and processed in similar fashion as a control. The uncultured SVY medium was assayed as another control, since it was likely that the SVY medium contained a measurable level of B6 vitamers. The results are shown in Table 2, below.

20 **Table 2: Production of B6 vitamers by *Bacillus subtilis* derivatives in 48 hour test tube cultures grown in SVY**

Strain	Cassette	Integration Target	OD ₆₀₀	Total B6 Vitamers ¹ mg/liter	Net B6 Vitamers ² mg/liter
PX14	$P_{26}yaaDE$	<i>yaaDE</i>	17	7.2	7.0
PX17	$P_{15}yaaDE$	<i>yaaDE</i>	17	4.9	4.7
PX1	$\Delta yaaDE$	<i>yaaDE</i>	8	0.4	0.2
PY79	-	-	19	0.8	0.6
(Medium)	-	-	0.08	0.2	(0)

¹ Sum of PN, PL, PM, and derivatives thereof that can be utilized by pyridoxine indicator strain *S. carlbergensis* as a source of vitamin B6 for growth.

25 ² Calculated by subtracting the amount assayed in the medium.

After subtracting the B6 vitamers contained in the medium, strain PX14 produced 7.0 mg/liter PL equivalents, while the parent PY79 produced only 0.6 mg/liter of PL equivalents. Thus, expression of the *yaaDE* operon has been shown to be rate limiting for B6 vitamer production in *B. subtilis*. Moreover, a genetically modified

30

strain, where this rate limiting step was enhanced, produced more than a ten-fold increase in B6 vitamers secretion compared to that of the parent.

EXAMPLE 5: Complementation of *E. coli* *pdx* mutants by plasmids that express the *B. subtilis* *yaaDE* operon.

5 Plasmid pDX14R, described above in Example 4, was used to transform various *E. coli* strains that contained mutations that lacked function in each of the known genes involved in PLP biosynthesis (except for *dxs*, which is an essential gene for *E. coli*). The selection was for resistance to 250 mg/liter ampicillin. Each transformant
10 was then tested for growth on minimal medium (SMM with 0.5 % glucose, see Example 2) supplemented with 100 mg/liter serine, and compared to growth of its respective untransformed parent on the same medium. All mutations tested were complemented by pDX14R. Specifically, *pdxA*, *pdxB*, *pdxF*, *pdxJ*, and *pdxH*, were all complemented by pDX14R. Therefore, expression of the *B. subtilis* *yaaDE* operon in *E. coli* is sufficient
15 for PLP biosynthesis, even in the absence of any one of the above functional *pdx* genes. Several important and unexpected conclusions or inferences can be drawn from these results. First, the substrate(s) for the enzyme(s) encoded by *yaaDE* must be present in *E. coli*, even when a biosynthetic intermediate normally used to make PLP is absent or greatly reduced. Second, PNP or PLP is possibly the product of the enzyme(s) encoded
20 by *yaaDE*. Third, since an early block in the *E. coli* PLP biosynthetic pathway (for example that in a *pdxB* mutant) does not prevent *yaaDE* from complementation, the substrates for the enzyme(s) encoded by *yaaDE* are not likely to be the same as for the last step in PNP or PLP synthesis in wild type *E. coli*. These unexpected results lead to the possibility of producing B6 vitamers using *B. subtilis* *yaaDE* or the homologous
25 genes from another organism (for example, but not limited to, *SOR* and *SNO* from *Cercospora nicotianae* or *PDX1* and *PDX2* from *S. cerevisiae*) in a heterologous host species, including, but not limited to, *E. coli* and *Oryza sativa*.

EXAMPLE 6: Overexpression of the *yaaDE* operon in *E. coli*.

30 Plasmids pDX14R and pDX17R were transformed into *E. coli* strain DH5 α (New England Biolabs), selecting for ampicillin resistance. The transformants were grown for 48 hours in 5 ml test tube cultures at 37°C, and the supernatants were worked up as in Example 3. The assay results for PL equivalents are shown in Table 3, below.
35

Table 3: Production of B6 vitamers by *Escherichia coli* harboring plasmids containing engineered *Bacillus subtilis* genes¹

Strain	Plasmid Cassette	OD ₆₀₀	Total B6 Vitamers ² mg/liter	Net B6 Vitamers ³ mg/liter
DH5α	<i>P₂₆yaaDE</i>	7.6	3.2	3.1
DH5α	<i>P₁₅yaaDE</i>	8.2	3.2	3.1
DH5α	-	9	0.1	(0)

¹ *E. coli* test tube cultures are grown in SVY for 48 hours.

² Sum of PN, PL, PM, and derivatives thereof that can be utilized by pyridoxine indicator strain *S. carlbergensis* as a source of vitamin B6 for growth.

³ Calculated by subtracting the amount assayed in DH5α not containing plasmid.

Thus it has been shown that the *yaaD* and *yaaE* genes can be expressed in a heterologous host strain, and B6 vitamers can still be overproduced. By extension of this approach, the *yaaD* and *yaaE* genes of *B. subtilis* can be overexpressed in any organism where an overexpression system exists, and in the resulting strains, B6 vitamers will be overproduced. Overproduction of the rate limiting enzyme for B6 vitamer production in any organism that is capable of producing B6 vitamers will lead to overproduction of B6 vitamers.

The YaaD and YaaE protein sequences were used as probes to search the NCBI database for homologs in plants using the BLAST™ program which can be found at the National Center for Biotechnology Information website (Altschul S.F (1990) *J. Mol. Biol.* 215(3):403-10). Several homologs of YaaD were found in several genera of plants, including *Arabidopsis*, *Oryza*, *Ginkgo*, *Hevea*, *Phaseolus*, and *Stellaria*. Two homologs of YaaE were found in *Arabidopsis thaliana*. However, no homologs of *pdxA* and *pdxJ* were found. Therefore the plant kingdom appears to use the Type B Pathway for B6 vitamer biosynthesis. Thus for example, overexpression of the YaaD homolog (GenBank accession number AAL73561) from *Oryza sativa* (rice), and the *A. thaliana* homolog of YaaE (GenBank accession number AB011483) together in a plant using methods well known in the art, such as expression from the Cauliflower Mosaic Virus 35S promoter, will lead to overproduction of B6 vitamers in that plant.

EXAMPLE 7: Other routes to increasing the activity of enzymes involved in B6 vitamer synthesis.

The overexpression of the *yaaDE* operon leads to an increase in the amount of the encoded enzyme(s), which in turn leads to an increase in the total activity of said enzyme(s). Increase in this activity leads to an increase in the production B6 vitamer. Other methods can be used to increase the activity of the relevant enzyme(s)

under conditions of B6 vitamer production. For example, in addition to increasing the amount of a relevant enzyme(s), the total activity of the relevant enzyme(s) can be increased by mutating the gene(s) to increase the specific activity of the enzyme(s), and/or by mutating the gene(s) to encode a feedback resistant variant of the enzyme(s).

- 5 Such desirable mutations can be obtained by screening large numbers of mutants for the increased activity as evidenced by an increase in B6 vitamer production as described in Example 4, or by selecting for mutants that are resistant to inhibitors that are specific for the PLP biosynthetic pathway, and screening among those mutants for an increase in B6 vitamer production. Examples of such inhibitors are isoniazid, iproniazid, and
- 10 ginkgotoxin (4'-methoxy pyridoxine) (Dempsey and Arcement (1971) J. Bacteriol. 107(2): 580-582; Pflug, W., and Lingens, F., (1978) Hoppe-Seyler's Z. Physiol. Chem. 359: 559-570; Fiehe, K., et al., (2000) J. Nat. Prod. 63(2): 185-189).

15 **EXAMPLE 8: Processing of biosynthetic B6 vitamers.**

- A B6 vitamer produced by a genetically modified organism of the invention can be harvested and processed into a format that is appropriate for commercial use. For example, after culturing a B6 vitamer producing micro-organism in liquid culture, the entire culture, including cells can be dried by evaporation or by spray
- 20 drying, and the resulting powder can be mixed into animal feeds. Alternatively, the cells can be first removed by centrifugation or filtration, and the resulting supernatant solution can be dried as described above. As another alternative, the B6 vitamer can be purified from the culture broth by techniques well known in the art, such as filtration, reverse osmosis, column chromatography (ion exchange, hydrophobic or hydrophilic
- 25 adsorption, gel filtration, etc.), solvent extraction, precipitation, distillation, evaporation, and the like. If the B6 vitamer producing organism is a plant, then the appropriate portion of the plant (for example the leaves, stems, roots, flowers, fruits, seeds, or any combination thereof) can be harvested and processed. For example the plant material can be dried and used directly, or the material can be pulverized or ground and the B6
- 30 vitamer extracted and/or processed as described above for cultures.

The production organism can be a micro-organism that normally inhabits the gut of humans or an animal of interest (for example one of many bacteria of the genus *Lactobacillus*, such as *L. acidophilus*), and the B6 vitamer can be delivered by ingestion of the organism.

35

60368618-032907
2005250-81989509

Equivalents

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

206220-0798909

What is claimed:

1. An organism that has been genetically modified to comprise a recombinant DNA molecule that results in the increase of the activity of one or more enzymes that catalyze(s) a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism.
2. The organism of claim 1, wherein B6 vitamer production is at least ten-fold higher than from the unmodified parent organism.
3. The organism of claim 1, wherein said enzyme is one or more of YaaD or YaaE.
4. The organism of claim 1, wherein said organism is genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer.
5. The organism of claim 4, wherein said genes are derived from *Bacillus*.
6. The organism of claim 4, wherein said genes are derived from *Bacillus subtilis*.
7. The organism of claim 4, wherein at least one of said genes is a *yaaD* gene.
8. The organism of claim 4, wherein at least one of said genes is a *yaaE* gene.
9. The organism of claim 4, wherein at least two of said genes are *yaaD* and *yaaE* genes.
10. The organism of claim 4, wherein said organism is a *Bacillus* strain.

202208190909

60366618-032002
20060220-187989209

11. The organism of claim 4, wherein said organism is *Bacillus subtilis*.
12. The organism of any one of claims 1-11, wherein said organism is grown in a liquid culture and the total B6 vitamer concentration in the culture supernatant is at least 7.0 mg/liter.
13. A method of producing a B6 vitamer comprising culturing a microorganism that has been genetically modified to overexpress one or more genes that encodes an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer, such that B6 vitamer production from said modified organism is increased compared to B6 production in an unmodified parent organism, under conditions such that the B6 vitamer is produced.
14. The method of claim 13, wherein said enzyme is one or more of YaaD or YaaE.
15. The method of claim 13, wherein at least one of said genes is a *yaaD* gene.
16. The method of claim 13, wherein at least one of said genes is a *yaaE* gene.
17. The method of claim 13, wherein said genes are contained on the *yaaDE* operon.
18. The method of claim 13, wherein the B6 vitamer is pyridoxine.
19. The method of claim 13, wherein the B6 vitamer is pyridoxal.
20. The method of claim 13, wherein the B6 vitamer is pyridoxamine.
21. The method of claim 13, wherein the said genes are bacterial-derived.
22. The method of claim 13, wherein said genes are derived from *Bacillus*.

23. The method of claim 13, wherein said genes are derived from *Bacillus subtilis*.
- 5 24. The method of claim 13, wherein the microorganism is Gram positive.
25. The method of claim 13, wherein the microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*,
10 *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.
26. The method of claim 13, wherein the microorganism is of the genus *Bacillus*.
- 15 27. The method of claim 13, wherein the microorganism is *Bacillus subtilis*.
28. The method of claim 13, further comprising recovering the B6 vitamer.
20
29. A method of producing a B6 vitamer comprising culturing a microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic gene under conditions such that the B6 vitamer is produced.
- 25 30. The method of claim 29, wherein the microorganism overexpresses at least one *Bacillus subtilis* B6 vitamer biosynthetic enzyme.
31. The method of claim 29, wherein the B6 vitamer is pyridoxine.
- 30 32. The method of claim 29, wherein the B6 vitamer is pyridoxal.
33. The method of claim 29, wherein the B6 vitamer is pyridoxamine.
34. The method of claim 29, wherein the microorganism
35 overexpresses at least two B6 vitamer biosynthetic enzymes.

60368618.032902
20062200-87-989809

60366618.032902

35. The method of claim 29, wherein the microorganism is Gram positive.
36. The method of claim 29, wherein the microorganism is Gram negative.
37. The method of claim 29, wherein the microorganism is a microorganism belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.
38. The method of claim 29, wherein the microorganism is of the genus *Bacillus*.
39. The method of claim 29, wherein the microorganism is *Bacillus subtilis*.
40. The method of claim 29, further comprising recovering the B6 vitamer.
41. A recombinant microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic gene.
42. A recombinant microorganism that overexpresses at least one *Bacillus* B6 vitamer biosynthetic enzyme.
43. The method of claim 42, wherein said enzyme is YaaD or YaaE.
44. The recombinant microorganism of claim 41 that overexpresses at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.
45. The recombinant microorganism of claim 41, wherein the B6 vitamer biosynthetic gene is selected from the group consisting of *yaaD* and *yaaE*.
46. The recombinant microorganism of claim 41, that is Gram positive.

47. The recombinant microorganism of claim 41 belonging to a genus selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci* and *Streptomyces*.

5 48. The recombinant microorganism of claim 41 belonging to the genus *Bacillus*.

49. The recombinant microorganism of claim 41 which is *Bacillus subtilis*.

10 50. A recombinant microorganism selected from the group consisting of PX14 and PX17.

51. A vector comprising a nucleic acid sequence that encodes at least one *Bacillus* B6 vitamer biosynthetic gene operably linked to regulatory sequences.

52. The vector of claim 51, comprising a nucleic acid sequence that encodes at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.

20 53. The vector of claim 51, wherein the regulatory sequences comprise a constitutively active promoter.

54. The vector of claim 51, wherein the constitutively active promoter comprises P_{15} (SEQ ID NO:9) or P_{26} (SEQ ID NO:10) sequences.

25 55. The vector of claim 51, wherein the regulatory sequences comprise at least one artificial ribosome binding site (RBS).

56. A vector selected from the group consisting of pDX14R and pDX17R.

57. A recombinant microorganism comprising the vector of claim 56.

58. An isolated nucleic acid molecule that encodes at least one *Bacillus* B6 vitamer biosynthetic gene.

50368618-032902

- 34 -

59. The isolated nucleic acid molecule of claim 58 that encodes at least one *Bacillus subtilis* B6 vitamer biosynthetic gene.

60. An isolated *Bacillus* B6 vitamer biosynthetic enzyme polypeptide.

61. An isolated *Bacillus subtilis* B6 vitamer biosynthetic enzyme polypeptide.

2062ED 81989ED9

**METHODS AND ORGANISMS FOR
PRODUCTION OF B6 VITAMERS**

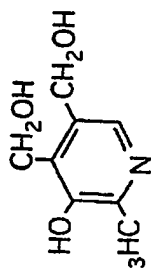
5 Abstract of the Disclosure

The present invention features methods of producing B6 vitamers that involve culturing an organism overexpressing an enzyme that catalyzes a step in the biosynthesis of a B6 vitamer under conditions such that a B6 vitamer is produced. The

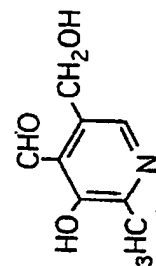
- 10 present invention further features methods of producing B6 vitamers that involve culturing recombinant microorganisms that overexpress at least one B6 vitamer biosynthetic gene, *e.g.*, *yaaD* or *yaaE*.

2006220 81989809

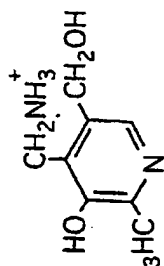
Figure 1



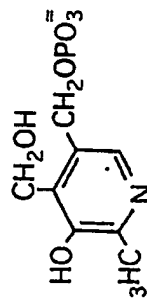
pyridoxol



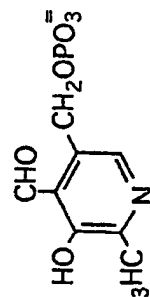
pyridoxal



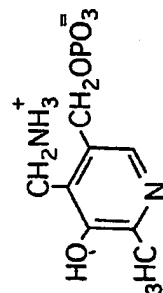
pyridoxamine



pyridoxol phosphate



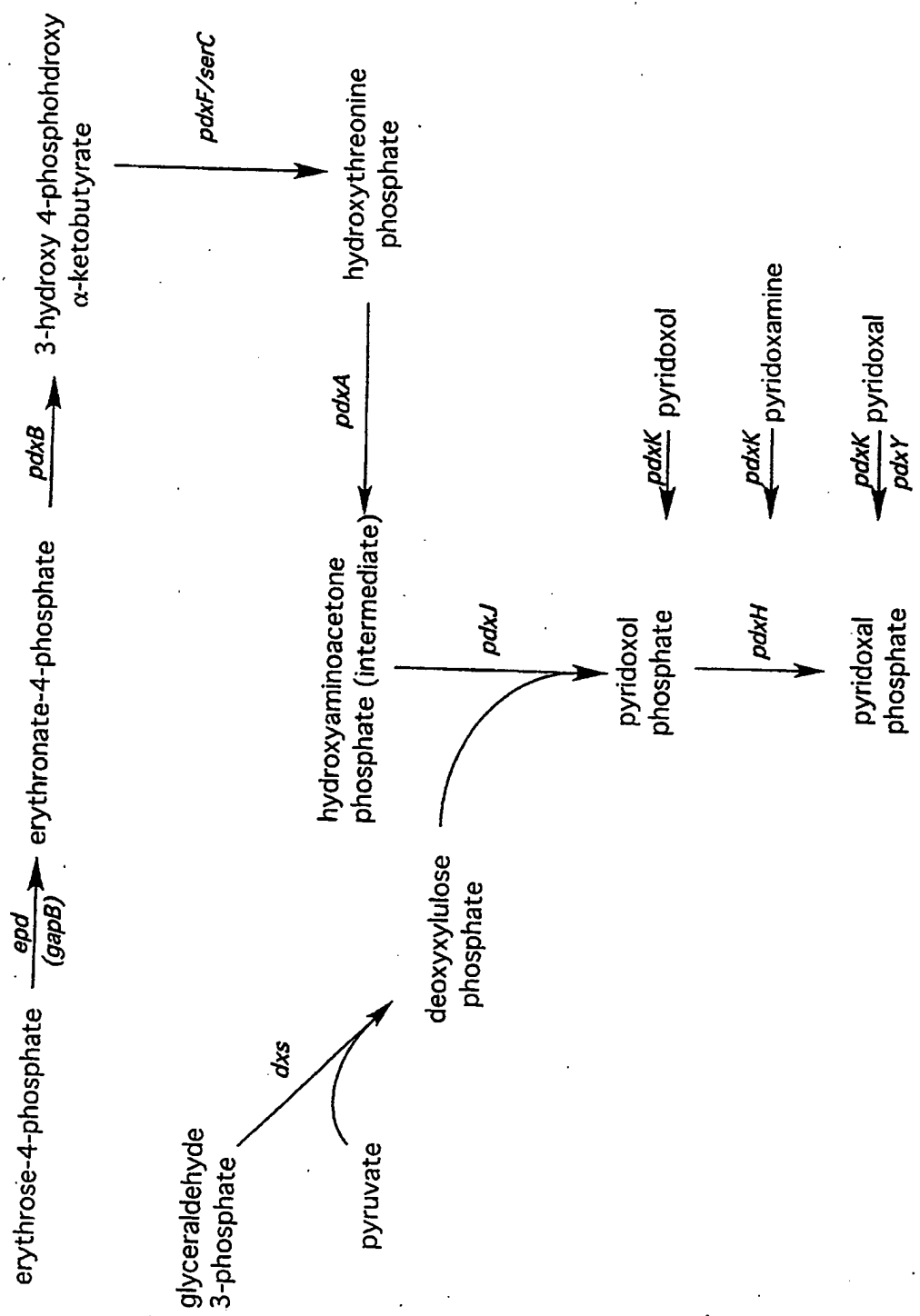
pyridoxal phosphate



pyridoxamine phosphate

201500181989A1

Figure 2



2006/22/01 18:19:59

Figure 3

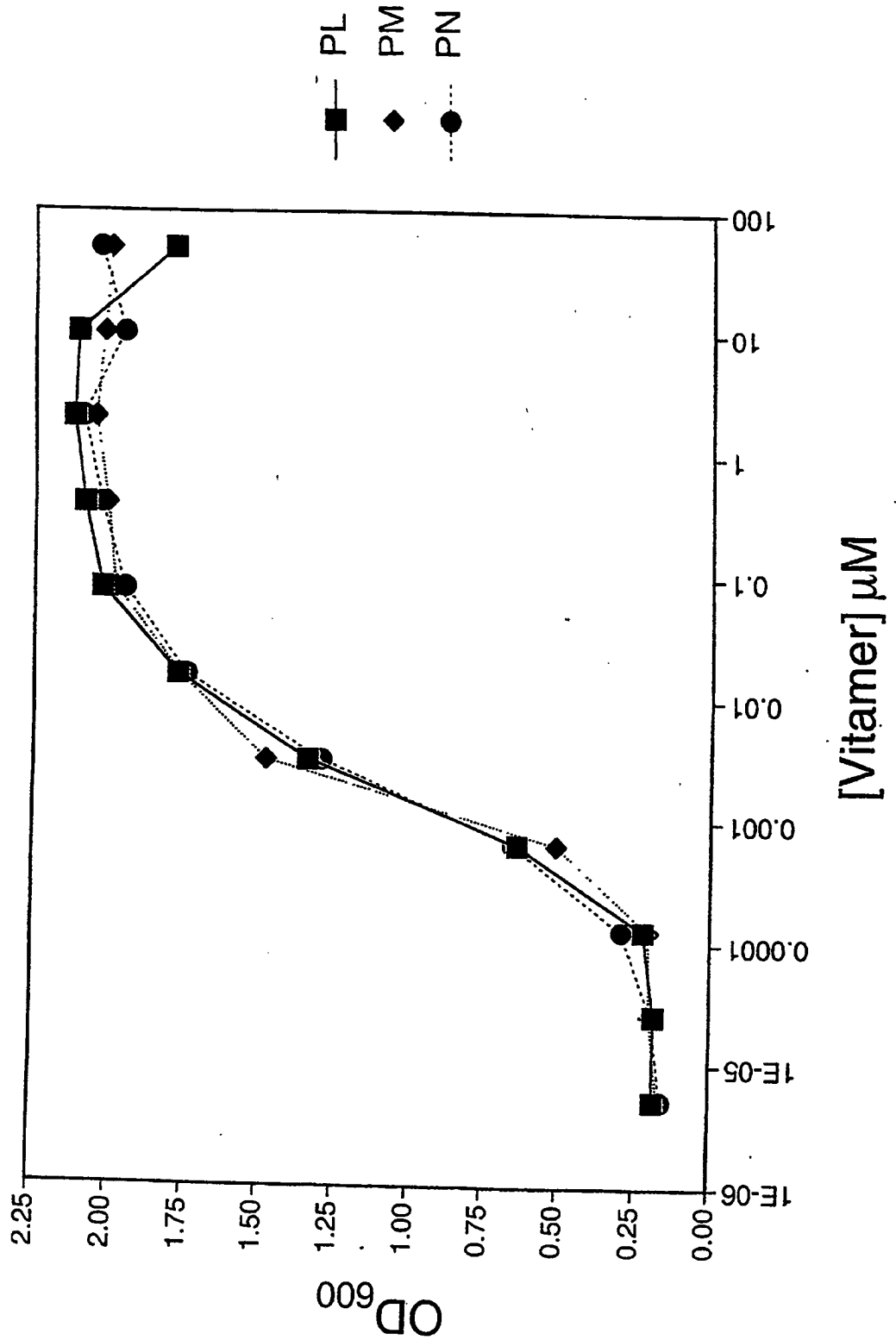


Figure 4. Structure of pDX1F

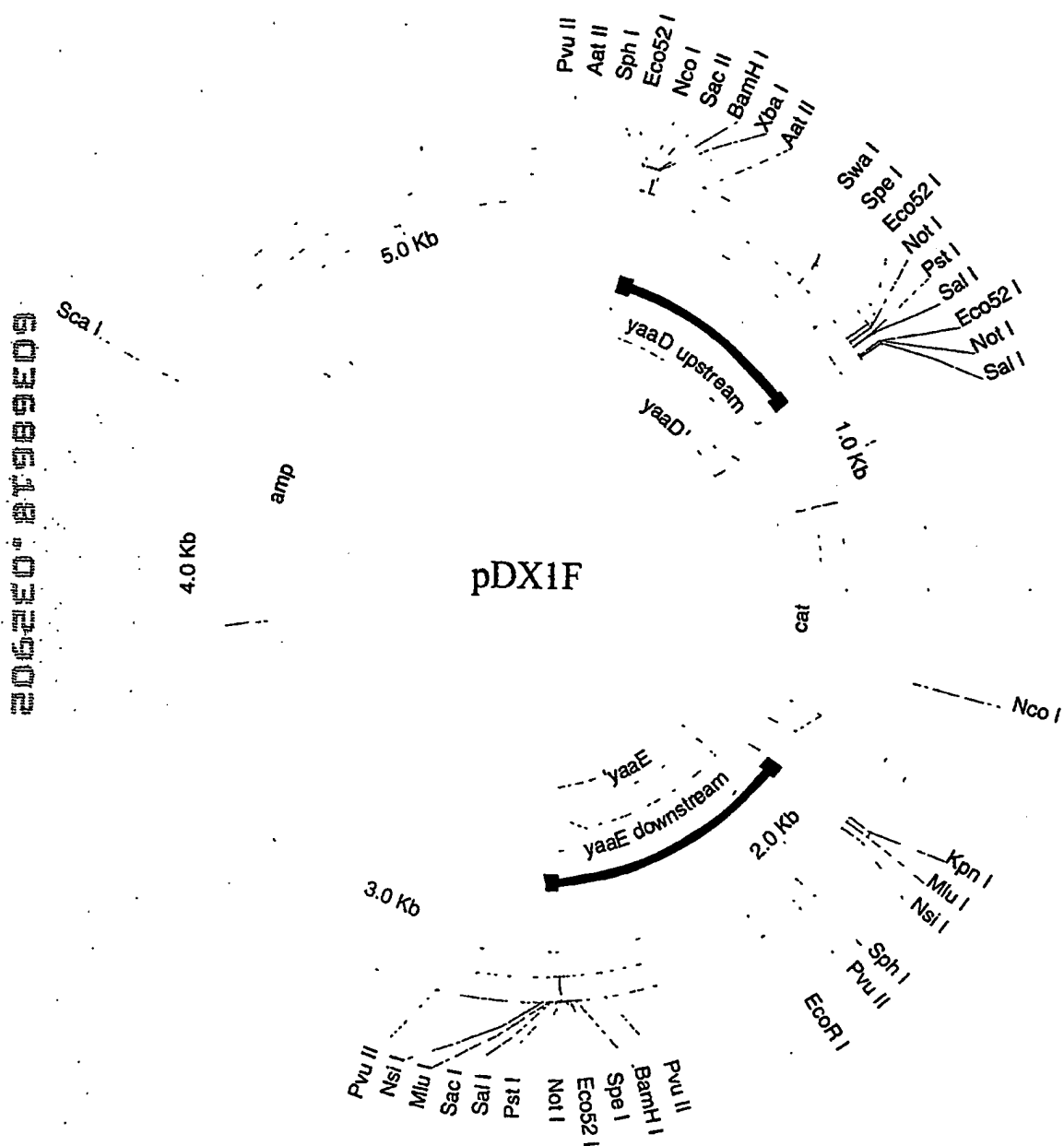


Figure 5. Structure of pDX11F

2062ED 07989209

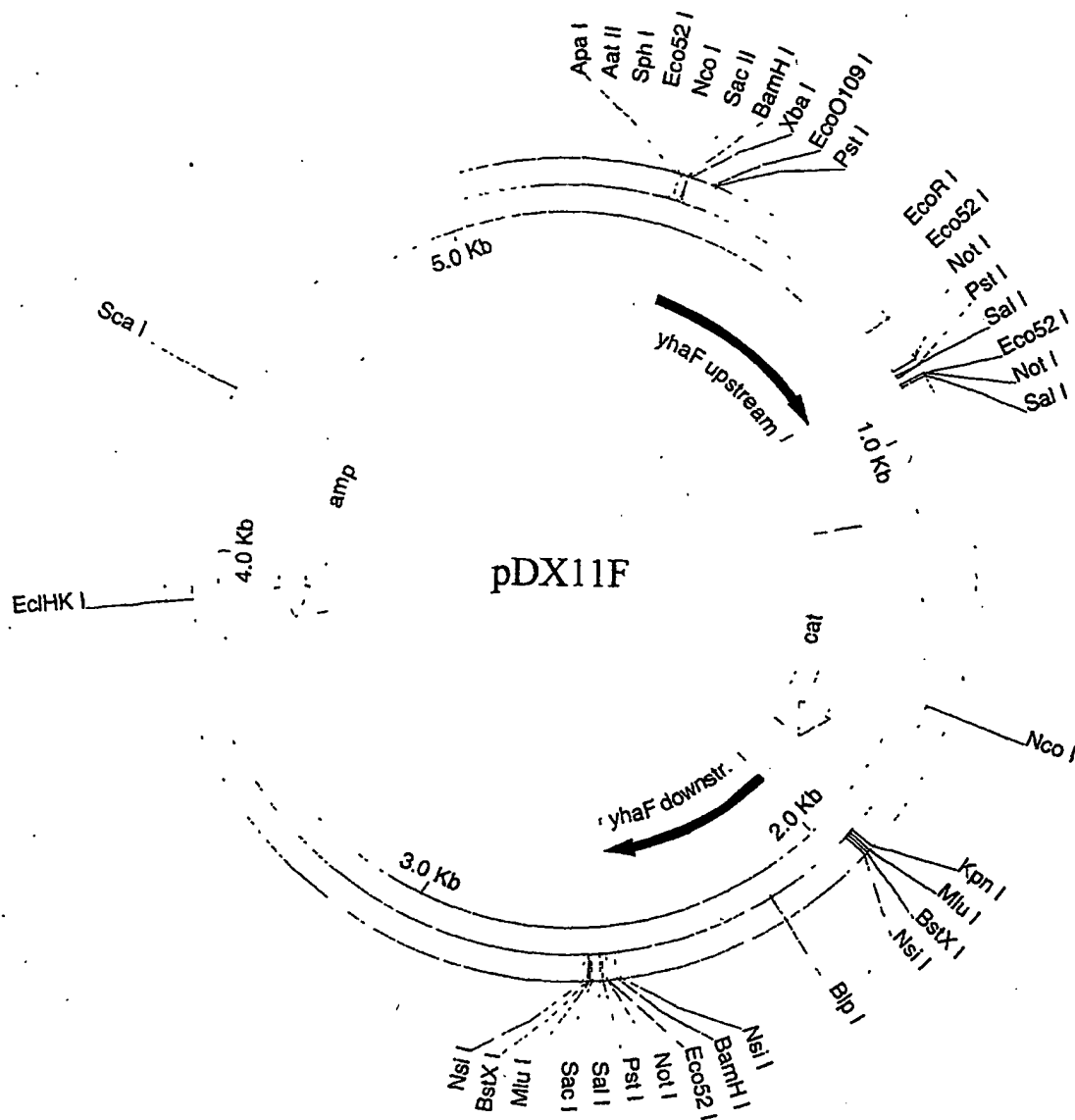


Figure 6

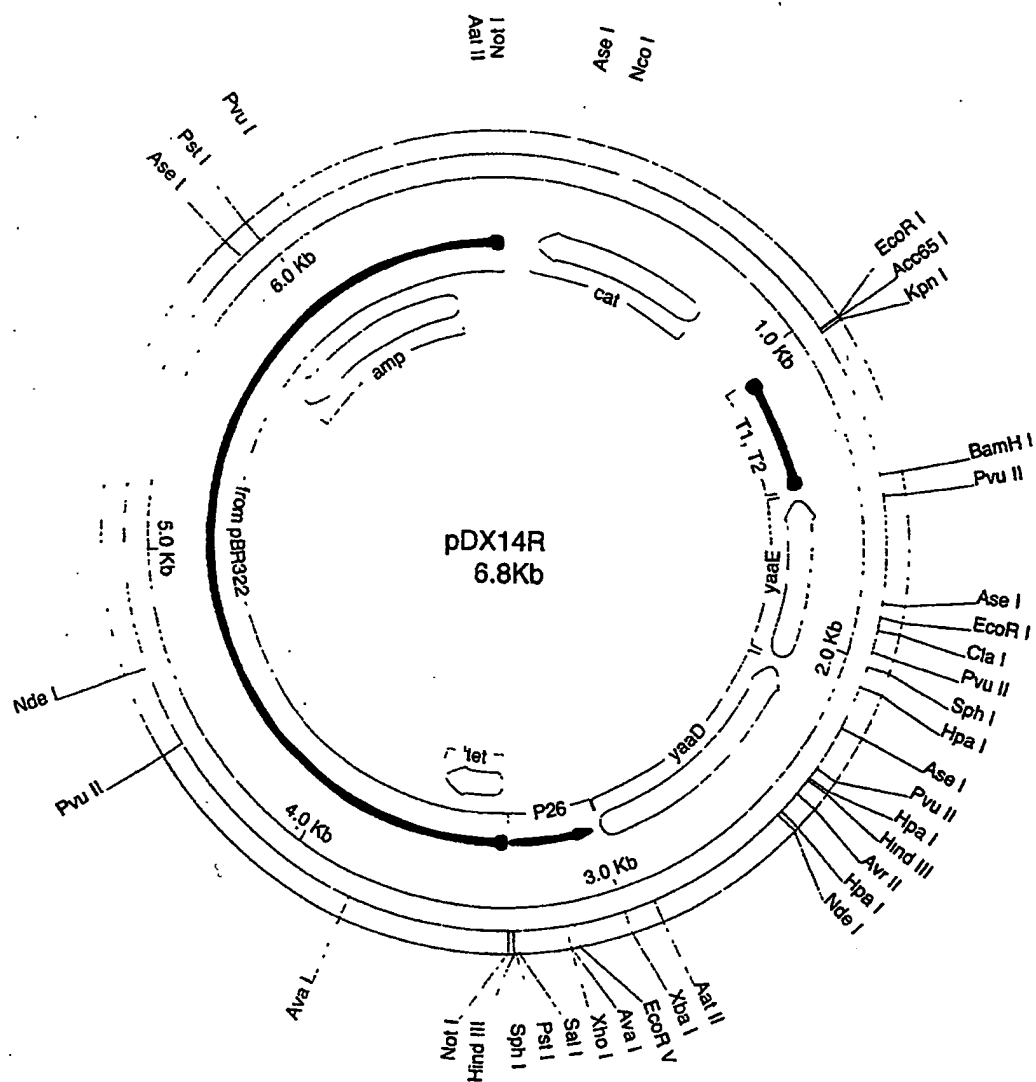
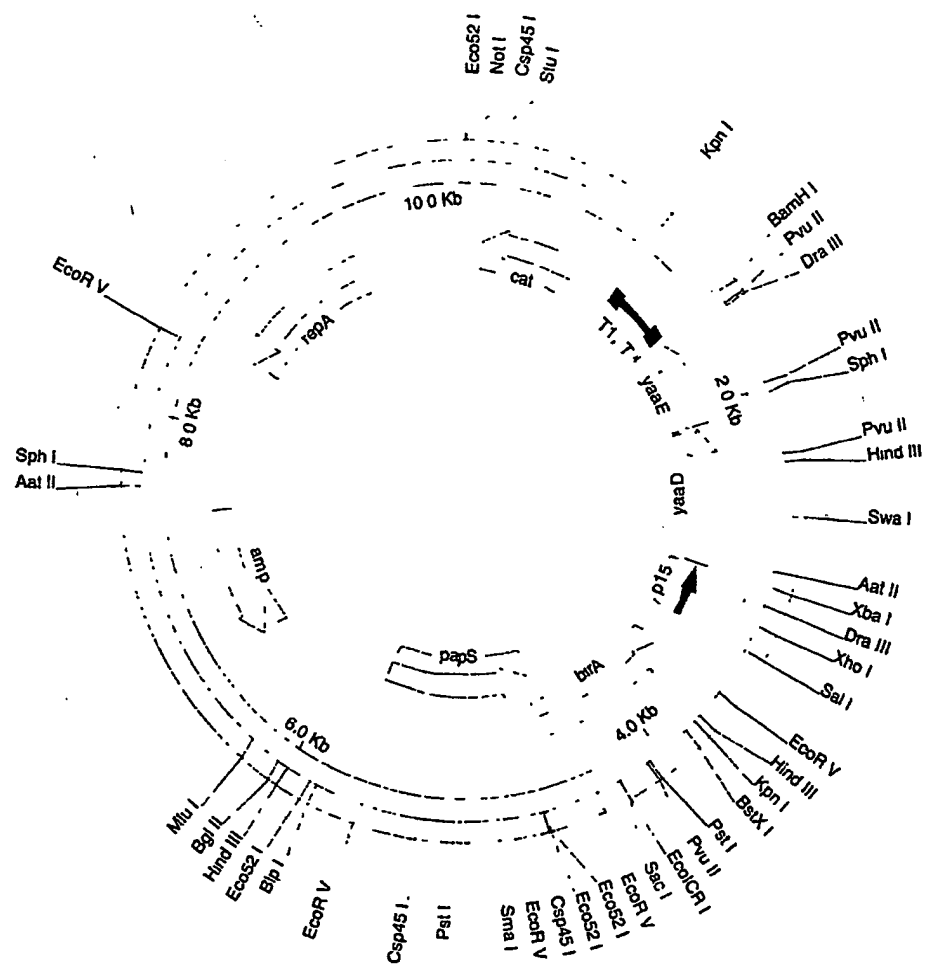


FIGURE 7. Structure of pDX17R



SEQUENCE LISTING

<110> Yocum, R. Rogers
Williams, Mark K.
Pero, Janice G.

<120> METHODS AND ORGANISMS FOR PRODUCTION OF B6 VITAMERS

<130> BGI-152-3

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 1

ccctctagag gaggagaaaa catggctcaa acaggtactg aacgtg

46

<210> 2

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 2

cccggatcct caactgtttt atacaagtgc cttttgotta tattc

45

<210> 3

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 3

ccctctagag gaggagacat aatggaacgt acaacgaatt ttaacgcag

49

<210> 4

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 4

cccggatccc ggacggtttg catagccaga ctttttactc a

41

<210> 5

<211> 5322

<212> DNA

SEQUENCE LISTING

<213> Artificial Sequence

<220>

<223> plasmid - pDX1F

<400> 5

50366619.0329002

tgcgcgcgcta	cagggcgcgt	coattcgcca	ttcaggctgc	gcaactgttg	ggaaggcgga	60
tcggtgcggg	cctcttcgct	attacgccag	ctggcgaaag	gggatgtgc	tgcaaggcga	120
ttaagtggg	taacgccag	gttttcccag	tcacgacgtt	gtaaaacgac	ggccagtga	180
ttgtaatacg	actcactata	ggcgcaattg	ggccgcagct	cgcatgctcc	cggccgccat	240
ggccgcggga	tccctctaga	ggaggagaaa	acatggctca	aacaggtaact	gaacgtgtaa	300
aacgcggaat	ggcagaaatg	caaaaaggcg	gcgtcatcat	ggacgtcatc	aatgcggaac	360
aagcgaaaaat	cgctgaagaa	gctggagctg	tcgctgtaat	ggcgctagaa	cgtgtgccag	420
cagatattcg	cgcggtgga	ggagttgccc	gtatggctga	ccctacaatc	gtggaagaag	480
taatgaatgc	agtatctatc	ccggtaatgg	caaaagcgcg	tatcgacat	attgttgaag	540
cgctgtgtct	tgaagctatg	ggtgttgact	atattgatga	aagtgaagtt	ctgacgccgg	600
ctgacgaaga	atttcattta	aataaaaatg	aatacacagt	tcctttttgtc	tgtgctgcc	660
gtgatcttgg	tgaagcaaca	cgccgtattg	cggaaagggtc	ttctatgctt	cgcacaaaag	720
gtgagcctgg	aacaggtaat	attgttgagg	ctgttcgcca	tatgcgtaaa	gttatcacta	780
gtgcggcgcg	ctgcaggctc	accatatggg	agaggcgcc	gcgtcgacca	atagttaccc	840
ttattatcaa	gataagaaag	aaaaggattt	ttcgctacgc	tcaaatacctt	taaaaaaaca	900
caaaagacca	catttttttaa	tgtggtcttt	attcttcaac	taaagcacc	attagttcaa	960
caaacgaaaa	ttggataaag	tgggatattt	ttaaaatata	tatttatgtt	acagtaatat	1020
tgacttttaa	aaaaggattg	attctaata	agaaagcaga	caagtaagcc	tcctaaattc	1080
actttagata	aaaatttagg	aggcatatca	aatgaacttt	aataaaattg	atttagacaa	1140
ttggaagaga	aaagagatat	ttaatcatta	tttgaaccaa	caaacgactt	ttagtataac	1200
cacagaaatt	gatattagtg	ttttataccg	aaacataaaa	caagaaggat	ataaatttta	1260
ccctgcattt	attttcttag	tgacaagggt	gataaactca	aatacagctt	ttagaactgg	1320
ttacaatagc	gacggagagt	taggttattg	ggataagtta	gagccacttt	atacaatttt	1380
tgatgggtga	tctaaaacat	tctctggtat	ttggactcct	gtaaagaatg	acttcaaaga	1440
gtttttatgat	ttataccttt	ctgatgtaga	gaaatataat	ggttcgggga	aattgtttcc	1500
caaaacacct	atacctgaaa	atgctttttc	tctttctatt	attccatgga	cttcattttac	1560
tgggtttaac	ttaaatatca	ataataatag	taattacctt	ctaccatta	ttacagcagg	1620
aaaattcatt	aataaaggta	attcaatata	tttaccgcta	tctttacagg	tacatcattc	1680
tgtttgtgat	ggttatcatg	caggattggt	tatgaactct	atccaggaat	tgtcagatag	1740
agcttaatgac	tgccttttat	aatatgagat	aatgccagct	gtacttttta	cagtcggttt	1800
tctaattgtca	ctaacctgcc	cgtttagtgt	aagaagggtt	ttatattaca	gctccgttac	1860
cgggctccca	acgcgttga	tgcatagctt	gagttattct	tagtgtcacc	taaatagctt	1920
ggcgtaatac	tggtcatagc	tgtttcctgt	gtgaaattgt	tatccgaaca	ataggtgtac	1980
taggacttca	aggagcagtt	agagagcaca	tccatgogat	tgaagcatgc	ggcgcggtcg	2040
gtctgtgctg	aaaacgtccg	gagcagctga	acgaagtga	cgggttgatt	ttgcccggcg	2100
gtgagagcac	gacgatgcgc	cgtttgatcg	atacgtatca	attcatggag	ccgcttcgtg	2160
aattcgctgc	tcagggcaaa	ccgatgtttg	gaacatgtgc	cggattaatt	atattagcaa	2220
aagaaattgc	cggttcagat	aatcctcatt	taggtcttct	gaatgtggtt	gtagaacgta	2280
attcatttgg	ccggcagggt	gacagctttg	aagctgattt	aacaattaaa	ggcttggacg	2340
agccttttac	tggggtattc	atccgtgctc	cgcatatttt	agaagctggt	gaaaatgttg	2400
aagttctatc	ggagcataat	ggtcgtattg	tagccgcgaa	acaggggcaa	ttccttggtc	2460
gctcattcca	tccggagctg	acagaagatc	accgagtgac	gcagctgttt	gttgaaatgg	2520
ttgaggaata	taagcaaaaag	gcacttgtat	aaaacagttg	aggatccggg	atcactagtg	2580
cggccgcctg	caggtcgacc	atatgggaga	gctcccaacg	cggttgatgc	atagcttgag	2640
tattctatag	tgtcacctaa	atagcttggc	gtaatcatgg	tcatagctgt	ttcctgtgtg	2700
aaattgttat	ccgctcacaa	ttccacacaa	catacagacc	ggaagcataa	agtgtaaagc	2760
ctggggtgcc	taatgagtga	gctaactcac	attaattgct	ttgcgctcac	tgcccgtttt	2820
ccagtcggga	aacctgtcgt	gccagctgca	ttaatgaatc	ggccaacgcg	cggggagagg	2880
cggtttgctg	attgggcgct	cttcgcgttc	ctcgtcact	gactcgctgc	gctcggtcgt	2940
tcggctgcgg	cgagcgggat	cagctcactc	aaaggcggtg	atacggttat	ccacagaatc	3000
aggggataac	gcaggaaaga	acatgtgagc	aaaaggccag	caaaaggcca	ggaaccgtaa	3060
aaaggccgcg	ttgctggcgt	ttttcgatag	gctccgcccc	cctgacgagc	atcacaaaaa	3120
tcgacgctca	agtcagaggt	ggcgaaaccc	gacaggacta	taaagatacc	aggcgttttc	3180
ccctggaagc	tcctcgtgc	tccgacctcg	ccgcttaccg	gatacctgtc	gatacctgtc	3240
cgcctttctc	ccttcgggaa	gcgtggcgct	ttctcatagc	tcacgctgta	ggatatctcag	3300

ttcggtgtag gtcgttcgct ccaagctggg ctgtgtgcac gaaccccccg ttcagcccga 3360
 ccgctgcgcc ttatccggtg actatcgtct tgagtccaac ccggtaaagac acgacttatc 3420
 gccactggca gcagccactg gtaacaggat tagcagagcg aggtatgtag gcggtgctac 3480
 agaattcttg aagtgggtgg ctaactacgg ctacactaga aggacagtat ttggtatctg 3540
 cgctctgctg aagccagtta ccttcggaaa aagagtttgt agctcttgat ccggcaaaaca 3600
 aaccaccgct ggtagcgtg gttttttgt ttgcaagcag cagattacgc gcagaaaaaa 3660
 aggatctcaa gaagatcctt tgatcttttc tacgggggtc gacgctcagt ggaacgaaaa 3720
 ctacagttaa gggatttttg tcatgagatt atcaaaaaag atcttcacct agatcctttt 3780
 aaattaaaaa tgaagtttta aatcaatcta aagtatatat gagtaaactt ggtctgacag 3840
 ttaccaatgc ttaatcagtg aggcacctat ctacgcatc tgtctatttc gttcatccat 3900
 agttgcctga ctccccgtcg ttagataaac tacgatacgg gagggcttac catctggccc 3960
 cagtgcctga atgataccgc gagaccacag ctacccggct ccagatttat cagcaataaa 4020
 ccagccagcc ggaaggggcg agcgcagaag tggctcctga actttatccg cctccatcca 4080
 gtctattaat tgttgccggg aagctagagt aagtagttcg ccagttaata gtttgcgcaa 4140
 cgttggtggc attgctacag gcatcgtggt gtcacgctcg tcgtttggta tggcttcatt 4200
 cagctccggg tcccaacgat caaggcgagt tacatgatcc cccatgttgt gcaaaaaagc 4260
 ggttagctcc ttcggctcctc cgatcgttgt cagaagtaag ttggccgcag tgttatcact 4320
 catggttatg gcagcactgc ataattctct tactgtcatg ccatccgtaa gatgcttttc 4380
 tgtgactggt gactactcaa ccaagtcatt ctgagaatac cgcgcccgcc gaccgagttg 4440
 ctcttgcccg gcgtcaatac gggataatag tgtatgacat agcagaactt taaaagtgtc 4500
 catcattgga aaacgttctt cggggcgaaa actctcaagg atcttaaccg tgttgagatc 4560
 cagttcgatg taaccactc gtgcacccaa ctgatcttca gcacttttta ctttcaccag 4620
 cgtttctggg tgagcaaaaa cagggaaggca aaatgccgca aaaaaggga taaggcgac 4680
 acggaaatgt tgaatactca tactcttctt ttttcaatat tattgaagca tttatcaggg 4740
 ttattgtctc atgagcggtt acatatattga atgtatttag aaaaataaac aaataggggt 4800
 tccgcgcaca tttccccgaa aagtgcaccc tgtatgcggt gtgaaatacc gcacagatgc 4860
 gtaaggagaa aataccgcat caggcgaaat tgtaaacgtt aatattttgt taaaattcgc 4920
 gttaaatatt tgttaaatca gctcattttt taaccaatag gccgaaatcg gcaaaatccc 4980
 ttataaatca aaagaataga ccagataggg gttgagtggt gttccagttt ggaacaagag 5040
 tccactatta aagaacgtgg actccaacgt caaaggcgca aaaaccgtct atcagggcga 5100
 tggccacta cgtgaaccat caccacaatc aagttttttg cggtcgaggt gccgtaaagc 5160
 tctaaatcgg aaccctaaag ggagcccccg atttagagct tgacggggaa agccggcgaa 5220
 cgtggcgaga aaggaaggga agaaagcgaa aggagcgggc gctagggcgc tggcaagtgt 5280
 agcgtgcacg ctgcgcgtaa ccaccacacc cgccgcgctt aa 5322

<210> 6
 <211> 5297
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> plasmid - pDX11F

<400> 6
 tgcgccgcta cagggcgct ccattcgcca ttcaggctgc gcaactgttg ggaaggcgca 60
 tcggtgcggg cctcttcgct attacgccag ctggcgaaag ggggatgtgc tgcaaggcga 120
 ttaagttggg taacgccagg gttttccag tcacgacgtt gtaaaacgac ggccagtga 180
 ttgtaatac actcactata gggcgaattg ggcccgacgt cgcattgctc cggccgccat 240
 ggcccgagg ggcctctaga ggaggagaca taatggaacg tacaacgaat ttaacgcag 300
 gtctgcagc gctgccactg gaagtctctc aaaaagcaca gaaagaattt attgatttta 360
 acgaatccgg catgtctgtt atggagcttt cccaccgcag caaagagtat gaagcgggtc 420
 accaaaaagc gaaaagcctc ttaatcgaa tgatgggcat tocggagat tacgatattc 480
 tgtttcttca aggcggggca agccttcaat tctcaatgct tccgatgaac tttttaacac 540
 ctgaaaaaac cgcacatttt gtgatgaccg gcgcttggtc tgaaaaagca ctggcagaaa 600
 cgaaaactgt cggaacacg tctatcacgg ctacaagtga aacagacaat tacagttata 660
 ttccagaggt tgaccttacg gatgtaaaag acggcgcata ttacatatc acatccaaca 720
 atacaatttt cggcactcag tggcaggagt ttccgaattc tccaattccg ctctgagccg 780
 acatgtccag cgtatatttt agcagaaaaa tcgatgtgtc caaatttgat gtgatctacg 840
 gaggcatcac tagtgccggc gctgcagggt cgaccatatg ggagaggcgg ccgcgtcgac 900

50363518-032902

caatagttac	ccttattatc	aagataagaa	agaaaaggat	ttttcgctac	gctcaaatcc	960
tttaaaaaaa	cacaaaagac	cacatttttt	aatgtgggtc	ttattcttca	actaaagcac	1020
ccattagttc	aacaaacgaa	aattggataa	agtgggatat	ttttaaaata	tatatattatg	1080
ttacagtaat	attgactttt	aaaaaaggat	tgattctaata	gaagaaagca	gacaagtaag	1140
cctcctaaat	tcacttttaga	taaaaattta	ggaggcatat	caaatgaact	ttaataaaat	1200
tgatttagac	aattggaaga	gaaaagagat	atttaatcat	tatttgaacc	aacaacagac	1260
ttttagtata	accacagaaa	ttgatattag	tgttttatac	cgaaacataa	aacaagaagg	1320
atataaattt	taccctgcat	ttattttcct	agtgacaagg	gtgataaact	caaatcacgc	1380
ttttagaact	ggttacaata	gcgacggaga	gtagggttat	tgggataagt	tagagccact	1440
ttatacaatt	tttgatgggtg	tatctaaaac	attctctggg	atttggactc	ctgtaaagaa	1500
tgacttcaaa	gagttttatg	attttacott	ttctgatgta	gagaaatata	atggttcggg	1560
gaaattgttt	cccaaaacac	ctatacctga	aaatgctttt	tctctttcta	ttattccatg	1620
gacttcattt	actgggttta	acttaaatat	caataataat	agtaattacc	ttctacccat	1680
tattacagca	ggaaaattca	ttaataaagg	taattcaata	tatttaccgc	tatctttaca	1740
ggtacatcat	tctgtttgtg	atggttatca	tgcaggattg	tttatgaact	ctattcagga	1800
attgtcagat	aggcctaagt	actggctttt	ataatatgag	ataatgccga	ctgtactttt	1860
tacagtcggg	tttctaattg	cactaacctg	ccccgttagt	tgaagaagg	ttttatatta	1920
cagctccggg	accgggctcc	caacgcgttg	gatgcatagc	ttgagtattc	tatagtgtca	1980
cctaaatagc	ttggcgtaat	catggtcata	gctgtttcct	gtgtgaaatt	gttatccgta	2040
gtcatcatga	aaaaaagctg	gctgcaaaat	gaaaatgcga	acgtcccaaa	aatcttgaaa	2100
tattccacgc	atgtcaaagc	ggattcactc	tacaacactc	cgccgacatt	tgcgatttat	2160
atgctgagcc	tcgttctgga	atggctcaag	gaaaacggcg	gtgtggaagc	tggtgaacag	2220
cgcaatgaac	aaaaagcgca	ggttctctac	agctgtattg	atgaaagcaa	cggcttctat	2280
aaaggacatg	ccagaaaaga	cagccgctca	cgcatgaatg	tcacattcac	gcttcgggat	2340
gacgaattaa	cgaaaacatt	ogttcagaaa	gcaaaagatg	cgaagatgat	cggccttggc	2400
ggacaccggt	cgggtgggag	ctgccgcgct	tctatttata	acgcgggtctc	tctcgaagac	2460
tgtgaaaaat	tagctgcgtt	catgaagaaa	ttccagcagg	aaaatgagta	aaaagtctgg	2520
ctatgcattc	cgtccgggat	ccgggatcac	tagtgcggcc	gcctgcagg	cgaccatatg	2580
ggagagctcc	caacgcgttg	gatgcatagc	ttgagtattc	tatagtgtca	cctaaatagc	2640
ttggcgtaat	catggtcata	gctgtttcct	gtgtgaaatt	gttatccgct	cacaattcca	2700
cacaacatac	gagccggaag	cataaagtgt	aaagcctggg	gtgcctaata	agtgaagtaa	2760
ctcacattaa	ttgcgttgcg	ctcactgccc	gctttccagt	cgggaaacct	gtcgtgccag	2820
ctgcattaat	gaatcggcc	acgcgcgggg	agaggcggtt	tgcgatttgg	gcgctcttcc	2880
gcttctcgc	tcactgactc	gctgcgctcg	gtogttcggc	tgccgcgagc	ggtatcagct	2940
cactcaaagg	cggtaatacg	gttatccaca	gaatcagggg	ataacgcagg	aaagaacatg	3000
tgagcaaaag	gccagcaaaa	ggccaggaac	cgtaaaaagg	ccgcgttgct	ggcgtttttc	3060
gataggctcc	gccccctga	cgagcatcac	aaaaatcgac	gctcaagtca	gaggtggcga	3120
aacccgacag	gactataaag	ataccaggcg	tttccccctg	gaagctccct	cgtgcgctct	3180
cctgttcoga	ccctgccgct	taccggatac	ctgtccgctt	ttctcccttc	gggaagcgtg	3240
cgcgctttctc	atagctcacg	ctgtaggtat	ctcagttcgg	tgtaggtcgt	tcgctccaag	3300
ctgggctgtg	tgacgaacc	ccccgttcag	cccgcacgct	gcgccttata	cggtaactat	3360
cgtcttgagt	ccaacccggg	aagacacgac	ttatcgccac	tggcagcagc	cactggtaac	3420
aggattagca	gagcgaggta	tgtaggcggt	gctacagagt	tcttgaagtg	gtggcctaac	3480
tacggctaca	ctagaaggac	agtatttggg	atctgcgctc	tgctgaagcc	agttaccttc	3540
ggaaaaagag	ttggtagctc	ttgatccggc	aaacaaacca	ccgctggtag	cgggtggttt	3600
tttgtttgca	agcagcagat	tacgcgcaga	aaaaaaggat	ctcaagaaga	tcctttgatc	3660
ttttctacgg	ggtctgacgc	tcagtggaac	gaaaactcac	gttaagggat	tttggtcatg	3720
agattatcaa	aaaggatctt	cacctagatc	cttttaaat	aaaaatgaag	ttttaaatca	3780
atctaaagta	tatatgagta	aacttggctt	gacagttacc	aatgcttaat	cagtgaaggca	3840
cctatctcag	cgatctgtct	atttcgttca	tccatagttg	cctgactccc	cgtcgtgtag	3900
ataactacga	tacgggaggg	cttaccatct	ggccccagtg	ctgcaatgat	accgcgagac	3960
ccacgctcac	cggctccaga	tttatcagca	ataaaccagc	cagccggaag	ggccgagcgc	4020
agaagtggtc	ctgcaacttt	atccgcctcc	atccagtcta	ttaattgttg	ccgggaagct	4080
agagtaagta	gttcgccagt	taatagtttg	cgcaacgttg	ttggcattgc	tacaggcatc	4140
gtggtgtcac	gctcgtcggt	tgggtatggc	tcattcagct	ccggttccca	acgatcaagg	4200
cgagttacat	gatcccccat	gttgtgcaaa	aaagcgggta	gctccttcgg	tcctccgatc	4260
gttgcagaa	gtaagttggc	cgcagtgtta	tcactcatgg	ttatggcagc	actgcataat	4320
tcctcttagc	tcatgccatc	cgtaagatgc	ttttctgtga	ctgggtgagta	ctcaaccaag	4380
tcattctgag	aataccgcgc	ccggcgaccg	agttgctctt	gcccggcgtc	aatacgggat	4440
aatagtgtat	gacatagcag	aactttaaaa	gtgctcatca	ttggaaaacg	ttcttcgggg	4500
cgaaaaactct	caaggatctt	accgctgttg	agatccagtt	cgatgtaacc	cactcgtgca	4560

cccaactgat cttcagcatc ttttactttc accagcgttt ctgggtgagc aaaaacagga 4620
aggcaaaatg cgcgcaaaaaa ggggaataag ggcacacgga aatgttgaat actcatactc 4680
ttcctttttc aatattattg aagcatttat cagggttatt gtctcatgag cggatacata 4740
tttgaatgta tttagaaaaa taaacaaata ggggttccgc gcacatttcc cggaaaagtg 4800
ccacctgtat gcggtgtgaa ataccgcaca gatgcgtaag gagaaaatac cgcatacaggc 4860
gaaattgtaa acgttaatat tttgttaaaa ttgcggttaa atatttgta aatcagctca 4920
ttttttaacc aataggccga aatcggcaaa atcccttata aatcaaaaga atagaccgag 4980
atagggttga gtgtgtgtcc agtttggaac aagagtccac tattaagaa cgtggactcc 5040
aacgtcaaag ggcgaaaaaac cgtctatcag ggcgatggcc cactacgtga accatcacc 5100
aaatcaagtt ttttgcggtc gaggtgccgt aaagctctaa atcggaaacc taaagggagc 5160
ccccgattta gagcttgacg gggaaagccg gcgaacgtg cgagaaagga agggaagaaa 5220
gcgaaaggag cgggcgctag ggcgctggca agtgtagcgg tcacgctgcg cgttaaccacc 5280
acaccgcgcg cgcttaa 5297

<210> 7

<211> 6731

<212> DNA

<213> Artificial Sequence

<220>

<223> plasmid - pDX14R

<400> 7

ttgcggccgc ttcgaaagct gtaatatataa aaccttcttc aactaacggg gcaggttagt 60
gacattagaa aaccgactgt aaaaagtaca gtccgcatta tctcatatta taaaagccag 120
tcattaggcc tatctgacaa ttcctgaata gagttcataa acaatcctgc atgataacca 180
tcacaaacag aatgatgtac ctgtaaagat agcggtaaat atattgaatt acctttatta 240
atgaattttc ctgctgtaat aatgggtaga aggttaattac tattattatt gatatttaag 300
ttaaaccag taaatgaagt ccatggaata atagaaagag aaaaagcatt ttcagggtata 360
ggtgttttgg gaaacaattt ccccgaaacca ttatatctct ctacatcaga aagggtataaa 420
tcataaaact ctttgaagtc attctttaca ggagtcctaaa taccagagaa tgttttagat 480
acaccatcaa aaattgtata aagtggctct aacttatccc aataacctaa ctctccgtcg 540
ctattgtaac cagttctaaa agctgtattt gagtttatca cccttgtcac taagaaaaata 600
aatgcagggt aaaatttata tcttctctgt tttatgtttc ggtataaaac actaatatca 660
atttctgtgg ttatactaaa agtcgtttgt tggttcaaat aatgattaaa tatctctttt 720
ctcttccaat tgtctaaatc aattttatta aagttcattt gatatgcctc cttaaattttt 780
atctaaagtg aatttaggag gcttacttgt ctgctttctt cattagaatc aatccttttt 840
taaaagtcaa tattactgta acataaatat atattttaaa aatatcccat tttatccaat 900
tttcgtttgt tgaactaatg ggtgcttag ttgaagaata aagaccacat taaaaaatgt 960
ggtcttttgt gtttttttaa aggatttgag cgtagcgaaa aatccttttc tttcttatct 1020
tgataataag ggtaactatt gaattcggta ccaagagttt gtagaaacgc aaaaaggcca 1080
tccgtcagga tggccttctg cttaatttga tgcttgccag tttatggcgg gcgtcctgcc 1140
cgccaccctc cgggcggtg cttecgcaacg ttcaaactccg ctcccggcgg atttgtccta 1200
ctcaggagag cgttcaccga caaacaacag ataaaacgaa aggccagtc tttcgactga 1260
gcctttcggt ttatttgatg cctggcagtt ccctactctc gcatggggag accccacact 1320
accatcggcg ctacggcggt tcaactctga gttcggcatg gggtcagggt ggaccaccgc 1380
gctactgccg ccaggcaaat tctgttttat cagaccgctt ctgcgttctg atttaactctg 1440
tatcaggctg aaaatcttct ctcatccgcc aaaaacaggat cctcaactgt tttatacaag 1500
tgcttttgc ttatatctct caaccatttc aacaaacagc tgcgtcactc ggtgatcttc 1560
tgtcagctcc ggtatggaat agcagccaag gaattgcccc tgtttcgcg ctacaatacg 1620
accattatgc tccgatagaa cttcaacatt ttcaccagct tctaaaatat gcggagcacg 1680
gatgaatacc ccagtaaaag gctcgtccaa gcctttaatt gttaaatacag cttcaaagct 1740
gtcaacctgc cggccaaatg aattacgttc tacaaccaca ttcagaagac cttaaagagg 1800
attatctgaa ccggcaattt cttttgctaa tataattaat ccggcacatg ttccaaacat 1860
cggtttgccc tgagcagcga attcacgaag cggctccatg aattgatacg tatcgatcaa 1920
acggcgatc ctgctgctct caccgcccgg caaaatcaac cgtcaactt cgttcagctg 1980
ctccggagct tttacgacaa gaccagccgc gccgcatgct tcaatcgcat ggatgtgctc 2040
tctaactgct ctttgaagtc ctagtacacc tattgttaac atgtcagcag cgtcctatg 2100
ttcttaccag ccgcgttctt gcatacgtg ttctggaagt aagtttgaga tttcaatccc 2160

5036613.032905

2006220: 075959E0

tttcattgca	gtaccaagct	cttttgacaa	ctcagcgatt	aatttgtaat	cagtaaagtg	2220
agttgttgct	tccacaattg	ctttcgcaaa	tttagcaggg	ttgtctgatt	taaaaaatacc	2280
agaaccaaca	aatactccgt	cagcaccaag	ctgcatcatg	agagcagcat	cagctggagt	2340
tgctacgccg	ccagcggcaa	agttaacgac	aggaagcttg	ccgtcttttt	taatttgaag	2400
aagaagctcg	taaggagcac	ctagggtttt	cgcttctgtc	attagctcat	cctcactcat	2460
cgcaactact	ttgcgcactt	gagcggtaac	tttacgcata	tgcggaacag	cctcaacaat	2520
attacctgtt	ccaggctcac	cttttggtcg	aagcatagaa	gcaccttccg	caatacggcg	2580
tggtgttca	ccaagatcac	ggcagccaca	gacaaaagga	actgtgtatt	cattttttatt	2640
taaatgaaat	tcttcgtcag	ccggcgtcag	aacttcactt	tcatcaatat	agtcaacacc	2700
catagcttca	agcacacgcg	cttcaacaat	atgtccgata	cgcgcttttg	ccattaccgg	2760
gatatatact	gcattcatta	cttcttccac	gattgtaggg	tcagccatac	gggcaactcc	2820
tccagccgcg	cgaatatctg	ctggcacacg	ttctagcgcc	attacagcga	cagctccagc	2880
ttcttcagcg	attttcgctt	gttcgcgatt	gatgacgtcc	atgatgacgc	cgcttttttg	2940
cattttctgcc	attccgcggt	ttacacgttc	agtacctgtt	tgagccatgt	tttctcctcc	3000
tctagagcgt	cctgctgttg	ttaagattat	tataccacac	cttgtagata	aagtcaacaa	3060
ctttttgcaa	aatttttcag	gaatttttagc	agaggttgtt	ctggatgtag	aacaaaatc	3120
ctttccgctc	ttgtgctgtt	aggatatctt	tttggaagc	taggtaggcc	tcgagttatg	3180
gcagttggtt	aaaaggaaac	aaaaagaccg	ttttcacaca	aaacgggtct	tttcgatttc	3240
tttttacagt	cacagccact	tttgcaaaaa	ccggacagct	tcatgcctta	taactgctgt	3300
ttcggctgac	ctgcaggcat	gcaagcttcg	cgaagcggcc	gcccagcgca	ggctggatgg	3360
ccttcccat	tatgattctt	ctcgcttccg	gcccgcacgg	gatgcccgcg	ttgcaggcca	3420
tgctgtccag	gcaggtagat	gacgaccatc	agggacagct	tcaaggatcg	ctcgcggtcc	3480
ttaccagctt	aacttcgatc	actggaccgc	tgatcgtcac	ggcgatttat	gccgcctcgg	3540
cgagcacatg	gaacgggttg	gcatggattg	taggcgcgcg	cctatacctt	gtctgcctcc	3600
ccgcgttgcg	tcgcggtgca	tgagccgggg	ccacctcgac	ctgaatggaa	gccggcggca	3660
cctcgctaac	ggattcacca	ctccaagaat	tggagccaat	caattcttgc	ggagaactgt	3720
gaatgcgcaa	accaaccctt	ggcagaacat	atccatcgcg	tccgccatct	ccagcagccg	3780
caagcggcgc	atctcgggca	gcgttgggtc	ctggccacgg	gtgcgcatga	tcgtgtctct	3840
gtcgttgag	accggctag	gctggcgggg	ttgccttact	ggttagcaga	atgaatcacc	3900
gatacgcgag	cgaacgtgaa	gcgactgctg	ctgcaaaacg	tctgcgacct	gagcaacaac	3960
atgaatggtc	ttcggtttcc	gtgtttcgta	aagtctggaa	acgcggaagt	cagcgccctg	4020
caccattatg	ttccggatct	gcatcgcagg	atgctgctgg	ctaccctgtg	gaacacctac	4080
atctgtatta	acgaagcgct	ggcattgacc	ctgagtgtat	tttctctggt	cccgccgcac	4140
ccataccgce	agttgtttac	cctcacacag	ttccagtaac	cgggcatggt	catcatcagt	4200
aaaccgctac	gtgagcatcc	tctctogttt	catcggtatc	attaccccca	tgaacagaaa	4260
ttccccctta	cacggaggca	tcaagtgtac	aaacaggaaa	aaaccgccct	taacatggcc	4320
cgcttttatca	gaagccagac	attaacgctt	ctggagaac	tcaacgagct	ggacgcggat	4380
gaacaggcag	acatctgtga	atcgcttcac	gaccacgctg	atgagcttta	ccgcagctgc	4440
ctcgcgctgt	tcggtgatga	cggtgaaaac	ctctgacaca	tgagctccc	ggagacggtc	4500
acagcttgct	tgtaagcgga	tgccggggag	agacaagccc	gtcagggcgc	gtcagcggtg	4560
gttgggcggt	gtcggggcgc	agccatgacc	cagtcacgta	gcgatacgcg	agtgtatact	4620
ggcttaacta	tgccgcatca	gagcagattg	tactgagagt	gcaccatatg	cggtgtgaaa	4680
taccgcacag	atgcgtaagg	agaaaatacc	gcatcaggcg	ctcttcgctt	tcctcgctca	4740
ctgactcgct	gcgctcggtc	gttcggctgc	ggcgagcggt	atcagctcac	tcaaaggcgg	4800
taatacgggt	atccacagaa	tcaggggata	acgcaggaaa	gaacatgtga	gcaaaaggcc	4860
acccggtaag	caggaaccgt	aaaaaggccg	cggtgtgtgc	gtttttccat	aggctccgcc	4920
cccctgacga	gcatacacia	aatcgacgct	caagtcagag	gtggcgaaac	ccgacaggac	4980
tataaagata	ccaggcggtt	ccccctggaa	gctccctcgt	gcgctctcct	gttccgaccc	5040
tgccgcttac	cggataactg	tcgccttttc	tccttcgggg	aagcgtggcg	ctttctcata	5100
gctcacgctg	taggtatctc	agttcggtgt	aggctgttcg	ctccaagctg	ggctgtgtgc	5160
acgaaccccc	cgttcagccc	gaccgctgcg	ccttatccgg	taactatcgt	cttgagtcca	5220
acccggtaag	acacgactta	tcgccactgg	cagcagccac	tggtaacagg	attagcagag	5280
cgaggatgtg	aggcggtgct	acagagttct	tgaagtgggt	gcctaaactac	ggctacacta	5340
gaaggacagt	atgtgtatc	tgcgctctgc	tgaagccagt	taccttcgga	aaaagagttg	5400
gtagctcttg	atccggcaaa	caaaccaccg	ctggttagcg	tggttttttt	gtttgcaagc	5460
agcagattac	gcgcagaaaa	aaaggatctc	aagaagatcc	tttgatcttt	tctacggggt	5520
ctgacgctca	gtggaacgaa	aactcacggt	aagggttttt	ggtcatgaga	ttatcaaaaa	5580
ggatcttccac	ctagatcott	ttaaattaaa	aatgaagttt	taaatcaatc	taaagtatat	5640
atgagtaaac	ttggtctgac	agttaccaat	gcttaatcag	tgaggcacct	atctcagcga	5700
tctgtctatt	tcgttcatcc	atagttgcct	gactccccgt	cgtgtagata	actacgatac	5760
gggagggctt	accatctggc	cccagtgctg	caatgatacc	gcgagaccca	cgctcaccgg	5820

```

ctccagattt atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggctctg 5880
caactttatc cgcctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt 5940
cgccagttaa tagtttgccg aacgttggtg ccattgctgc aggcacgtg gtgtcacgct 6000
cgtcgtttgg tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat 6060
cccccatggt gtgcaaaaaa gcggttagct cttcgggtcc tccgatcgtt gtcagaagta 6120
agttggccgc agtggtatca ctcatggtta tggcagcact gcataattct cttactgtca 6180
tgccatccgt aagatgcttt tctgtgactg gtgagtactc aaccaagtca ttctgagaat 6240
agtgtatgcg gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac 6300
atagcagaac tttaaaagtg ctcatcattg gaaaaacgtt ttcggggcga aaactctcaa 6360
ggatcttacc gctgttgaga tccagttcga tgaacccac tcgtgcaccc aactgatctt 6420
cagcatcttt tactttcacc acggtttctg ggtgagcaaa aacaggaagg caaaatgccg 6480
caaaaaaggg aataagggcg acacggaagt gttgaatact catactcttc ctttttcaat 6540
attattgaag catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt 6600
agaaaaataa acaaataggg gttccgcgca catttccccg aaaagtgcc cctgacgtct 6660
aagaaaccat tattatcatg acattaacct ataaaaatag gcgtatcacg aggccctttc 6720
gtcttcaaga a 6731

```

<210> 8

<211> 10181

<212> DNA

<213> Artificial Sequence

<220>

<223> plasmid - pDX17R

<400> 8

```

gaattttgcg gccgcttoga aagctgtaat ataaaaacct tcttcaacta acggggcagg 60
ttagtgacat tagaaaaccg actgtaaaaa gtacagtcgg cattatctca tattataaaa 120
gccagtcatt aggcctatct gacaattcct gaatagagtt cataaacaat cctgcatgat 180
aaccatcaca aacagaatga tgtacctgta aagatagcgg taaatatatt gaattacctt 240
tattaatgaa ttttcctgct gtaataatgg gtagaaggta attactatta ttattgatat 300
ttaagttaaa ccagtaaat gaagtccatg gaataataga aagagaaaaa gcattttcag 360
gtataggtgt tttgggaaac aatttccccg aaccattata tttctctaca tcagaaaagg 420
ataaatcata aaactctttg aagtcattct ttacaggagt ccaaatacca gagaatgttt 480
tagatacacc atcaaaaatt gtataaagtg gctctaactt atcccaataa cctaactctc 540
cgtcgctatt gtaaccagtt ctaaaagctg tatttgagtt tatcaccctt gtcactaaga 600
aaataaatgc aggttaaaat ttatatcctt cttgttttat gtttcgggat aaaacactaa 660
tatcaatttc tgtggttata ctaaaagtcg tttgttggtt caaataatga ttaaataatt 720
cttttctctt ccaattgtct aaatcaattt tattaaagtt catttgatat gcctcctaaa 780
tttttatcta aagtgaattt agggaggctt cttgtctgct ttcttcatta gaatcaatcc 840
ttttttaaaa gtcaatatta ctgtaacata aatatatatt ttaaaaatat ccactttat 900
ccaattttcg tttgttgaa taatgggtgc tttagttgaa gaataaagac cacattaaaa 960
aatgtggtct tttgtgtttt tttaaaggat ttgagcgtag cgaaaaatcc ttttctttct 1020
tatcttgata ataagggtaa ctattgaatt cggtaaccaag agttttaga aacgcaaaaa 1080
ggccatccgt caggatggcc ttctgcttaa tttgatgcct gccagtttat ggcgggcgctc 1140
ctgcccgcga cctccgggc cggtgcttcg caacgttcaa atccgctccc ggcggtttg 1200
tctactcag gagagcgttc accgacaaac aacagataaa acgaaaggcc cagtctttcg 1260
actgagcctt tcgttttatt tgatgcctgg cagttcccta ctctcgcatg gggagacccc 1320
acactaccat cggcgctacg gcgtttcact tctgagttcg gcatggggtc aggtgggacc 1380
accgcgtac tgccgccagg caaattctgt tttatcagac cgcttctgcg ttctgattta 1440
atctgtatca ggctgaaaat cttctctcat ccgcaaaaac aggatcctca actgttttat 1500
acaagtgcct tttgcttata ttctcaacc atttcaacaa acagctgcgt cactcgggtg 1560
tcttctgtca gtcgggatg gaatgagcag ccaagggaatt gccctgttt cgcggttaca 1620
atacgaccat tatgctccga tagaacttca acattttcac cagcttctaa aatatgcgga 1680
gcacggatga ataccccgat aaaaggctcg tccaagcctt taattgttaa atcagcttca 1740
aagctgtcaa cctgcgggc aaatgaatta ogttctacaa ccacattcag aagacctaaa 1800
tgaggattat ctgaaccggc aatttctttt gctaataata ttaatccggc acatgttcca 1860
aacatcggtt tgccctgagc agcgaattca cgaagcggct ccatgaattg atacgtatcg 1920
atcaaacggc gcatcgctgt gctctcaccg cccggcaaaa tcaaccgctc aacttcgttc 1980

```

2025-01-03 15:03:03

60368618 031200

agctgctccg gacgttttac gacaagacca gccgcgccgc atgcttcaat cgcattggatg 2040
 tgctctctaa ctgctccttg aagtccctagt acacctattg ttaacatgtc agcagcgctc 2100
 ctatgtttctt accagcccgcg ttcttgacata cgctgttctg gaagtaagtt tgagatttca 2160
 atcccttttca ttgcagtacc aagctctttt gacaactcag cgattaattt gtaatcagta 2220
 aagtgaagttg ttgcttccac aattgctttc gcaaatttag cagggttgctc tgatttaaaa 2280
 ataccagaac caacaaatac tccgtcagca ccaagctgca tcatgagagc agcatcagct 2340
 ggagttgcta cgccgccagc ggcaaaagta acgacaggaa gcttgccgtc ttttttaatt 2400
 tgaagaagaa gctcgtaaag agcacctagg tttttcgctt ctgtcattag ctcatcctca 2460
 ctcatcgcaa ctactttgcg cacttgagcg ttaactttac gcatatggcg aacagcctca 2520
 acaatattac ctgttccagg ctacactttt gtgcgaagca tagaagcacc ttccgcaata 2580
 cggtgtgttg cttoaccaag atcacggcag ccacagacaa aaggaaactgt gtattcattt 2640
 ttattttaaat gaaattcttc gtcagccggc gtcagaactt cactttcatc aatatagtca 2700
 acacccatag cttcaagcac acgcgcttca acaatatgtc cgatacgcgc ttttgccatt 2760
 accgggatag atactgcatt cattacttct tcacagattg tagggtcagc catacgggca 2820
 actcctccag ccgcgcgaat atctgctggc acacgttcta gcgccattac agcgacagct 2880
 ccagcttctt cagcgatttt cgcttgcttc gcattgatga cgtccatgat gacgcgcctc 2940
 ttttgcaattt ctgccattcc gcgttttaca cgttcagtac ctgtttgagc catgttttct 3000
 cctcctctag aacaggcggg gttgcccccg ctgttaatta aattattaca caccctgtag 3060
 ggaaagtcaa tacctttttg taaaattttt acacagcgtg gatctcttct agggacacct 3120
 ctttgtagcc ctcaaggag aaatatggc ggtactgagc acagttttgg ttggtggaca 3180
 gtgaaccata gctgtcgtca atagcctcga gttatggcag ttggttaaaa ggaaacaaaa 3240
 agacggtttt cacacaaaac ggtctttttc gatttctttt tacagtcaca gccacttttg 3300
 caaaaaccgg acagcttcat gccttataac tgctgtttcg gtcgacgatg atctgcccgt 3360
 ttcttctgca agccaaaaaa ccttccgtta caacgagaag gattcttcac tttctaaagt 3420
 tcggcgagtt tcatcctct gtccagtcoc ttttttggat caaggcagac tgctgcaatg 3480
 tctatctatt ttaataatag gtgcagttcg caggcgatac tgcccaatgg aagtatacca 3540
 aaatcaacgg gcttgtagca acacattagc ccaattcgat atcggcagaa tagatttttt 3600
 taatgccttc gttcgtttct aaaagcagaa cgccttcac atctatacct aacgccttac 3660
 cgtaaaaggt tccggttaac gttctggctc tcatattagt gccaataccg agcgcatagc 3720
 tttcccataa aagottaatc ggcgtaaatc cgtgcgtcat ataatcccgg taccgtttct 3780
 caaagcatag taaaatatgc tggatgagc cgcccgatc aattttttcc ccagcagctt 3840
 ggctgaggct tgctgcgatg tcttcaatt catctggaat atcattaggc tgctgggttaa 3900
 cgttaatgac gatcccaatg atcactgaac gtacgcggtc ttcttcagcc tgcatttccg 3960
 ttggatgacc gactgttttt tttcogttaa tcaaaatate atttgccat ttaatatccg 4020
 tttggatgcc tgctgcctct tctattccct gcacaacagc tactgcagca agcagagta 4080
 gctgcggtgt tttttggagc ggaatgtcag gccgcaaaat caggctcatc caaacaccgt 4140
 ttcttctctg agaatgccat accctagaca ttccggccct tccggctgtt tgtttgcag 4200
 ccaccacaag ggtgccttcc ggtgcgttat tattcgcgag ctcatgagcc gttttttg 4260
 tgcttgaag aacgtcatgg taaataagat gctggcccat cacttccgtt tttaatccaa 4320
 aacgaatttc gctttcactg agttttcgg gttttttgat gagccgatc ccttttctc 4380
 taacggcttc tacttcataa cctcttttcc gaagctcttc aatatgcttc cacacagcag 4440
 ttcttgaaca gccgagagca tcaactgattt tttggccgga aataaattca ttgcccgcct 4500
 gagaaaataa ttcaataagg tcttttctta atgttgaccg catgtcttca gccactctc 4560
 tatgtgttcc ttttgattgg agagcttccc tgtcacaaca gcctgctcga tccactgtaa 4620
 ttcttctgac acccattttc cggccggccg gtttgaagc gcaagcaagt ccttaccctt 4680
 gatatacaaga tcttaaggc ttttgatcgg caggttttga taagcgtact gaatgtcctt 4740
 cagtttcttt tcatccagtt tttcgttttg ccgaagctgc gatattttgg ccgctgagag 4800
 cagtgttttt ttccagctc tgtacattgt cattgcgtca aggtctctggc caaacgtatc 4860
 ggcaatgtga atggcttctt tgatcacttt tcccgggagc ttccaggctt tcaggaaaag 4920
 gggcgcgctt ttcaaaaacta tgccaagggtt aattaaaaga gcagcccaaa gctcctcacg 4980
 ggaatgttaa gagaagaatg gaaactcact cgttgaaatc aggttttctc gtttatgata 5040
 aaaaccagga agctcttcat acaatctcgt ttgaatgagt gtttgaagcg cctggcgaga 5100
 agctcttccc tgcagcaatt tctcaaactc tatagttttt cgttcgactg aaacatggga 5160
 gaggagtgat ttttctttcg caatggcttc ttctgtttcc ggtgaaagcg taaagccaag 5220
 ctggctcata aagcgtacgg ctctcagcat acgaagcgca tctcttgtaa atctatctc 5280
 aggttttcca acggttcgaa tcaactttctg atcaatatct ttcttgccgc caaaataatc 5340
 aagcaccttc cgttcgctg tcatggccat cgcattgate gttaaatctc tgctgttttag 5400
 atcctcttct aatgatgaga taaattgcac tttctgacgt cttctgaaat caacataatc 5460
 agattcagtc cggaatgtcg tgacttcata ggtttcatcc tccagagca caataatgg 5520
 cccgtgctct ttgcctacat caacagtcog ctgaaacagc cgttctactt gatcaggtgc 5580
 cgcattctgt gcgatatcga catctccgat cgttctgttc atatagctgt cacgaactgc 5640

50368618.032902

gccccgcaca aaataagcct gatggccgcg ttcgattaag atgcggagca cgggaagtgc 5700
 tttgataaaa actttttcca tgtgatcact ccggttctgc taaatcggca taaatctgtt 5760
 catactggct gacaattttt ttagaagaaa attcattttc aagcatctct attgccgcct 5820
 ttgtaaaacg attgcttagc tgttcattctt ctaaaatgct catcgcgcg gctgtttgcg 5880
 ccgtaacatc accgacatcc accaaaaatc cgctcacatt gttttttata acctcaggga 5940
 taccgccaat gtttgttcca atacaaggca ctccgcaagc catcgcttca agcaggacaa 6000
 ggccaaagct ttctttttca gatagcagca gcttcaaato gctaatagaa taaagatctt 6060
 caacacggtc ttgattttcca agcattaaga cttgggtcttc caagccatat tttctgataa 6120
 gctcgagcgc tgtcgatttc tccggaccgt ctccgactaa aagcagcttc gctttcgttt 6180
 tgcacgcgat attgcggaac acacggatga catcctgcac gcgtgcagcc actgggtaaca 6240
 ggattagcag agcaggtat gttagcggtg ctacagagt cttgaagtgg tggcctaact 6300
 acggctacac tagaaggaca gtatttggtt tctgcgctct gctgaagcca gttaccttcg 6360
 gaaaaagagt tggtagctct tgatccggca aacaaaccac cgctggtagc ggtggttttt 6420
 ttgtttgcaa gcagcagatt acgcgcagaa aaaaaggatc tcaagaagat cctttgatct 6480
 tttctacggg gtctgacgct cagtggaaacg aaaactcacg ttaagggtatt ttggtcatga 6540
 gattatcaaa aaggtatctt acctagatcc ttttaaatta aaaatgaagt tttaaatcaa 6600
 tctaaagtat atatagtaa acctggtctg acagttacca atgcttaatc agtgaggcac 6660
 ctatctcagc gatctgtcta tttcgttcat ccatagttgc ctgactcccc gtcgtgtaga 6720
 taactacgat acgggagggc ttaccatctg gccccagtgc tgcaatgata ccgcgagacc 6780
 cacgctcacc ggctccagat ttatcagcaa taaaccagcc agccggaagg gccgagcgca 6840
 gaagtggctc tgcaacttta tccgcctcca tccagtctat taattgttgc cgggaagcta 6900
 gagttaagtag ttcgccagtt aatagtttgc gcaacgttgt tgccattgct acaggcatcg 6960
 tgggtgtcacg ctogtcgttt ggtatggctt cattcagctc cggttcccaa cgatcaaggc 7020
 gagttacatg atcccccatg ttgtgcaaaa aagcggttag ctctctcggc cctccgatcg 7080
 ttgtcagaag taagttggcc gcagtgttat cactcatggt tatggcagca ctgcataatt 7140
 ctcttactgt catgccatcc gtaagatgct tttctgtgac tggtagtac tcaaccaagt 7200
 cattctgaga atagtgtatg cggcgaccga gttgctcttg cccggcgtca atacgggata 7260
 ataccgcgcc acatagcaga actttaaaag tgctcatcat tggaaaacgt tcttcggggc 7320
 gaaaactctc aaggatctta ccgctgttga gatccagttc gatgtaaccc actcgtgcac 7380
 ccaactgac ttcatcatct tttactttca ccagcgttto tgggtgagca aaaacaggaa 7440
 ggcaaaatgc cgcaaaaaag ggaataaggc cgacacggaa atgttgataa ctcatactct 7500
 tcttttttca atattattga agcattttatc agggttattg tctcatgagc ggatacatat 7560
 ttgaatgtat ttagaaaaat aaacaatatg gggttccgcg cacatttccc cgaaaagtgc 7620
 catctgacgt ctaagaaaacc attattatca tgacattaac ctataaaaat aggcgtatca 7680
 cgaggccctt tegtctcgca tgcggatcag tgagggtttg caactgcggg tcaaggatct 7740
 ggatttogat cacggcacga tcatcgtgcg ggagggcaag ggctccaagg atcgggacct 7800
 gatgttacct gagagcttgg caccagcct gcgcgagcag gggaattgat ccggtggatg 7860
 accttttgaa tgacctttaa tagattatat tactaattaa ttggggagccc tagaggctcc 7920
 tctttttatt ttaaaaattt tttcacaaaa cggtttacaa gcataacggg ttttgcgtcc 7980
 cgcaaacggg ctgttctggt gttgctagtt tgttatcaga atcgagatc cggtctcagg 8040
 tttgcggct gaaagcgcta tttctccag aattgccatg atttttccc cacgggaggc 8100
 gtcactggct ccggtgttgt cggcagcttt gattcgataa gcagcatcgc ctgtttcagg 8160
 ctgtctatgt gtgactgttg agctgtaaca agttgtctca ggtgttcaat ttcatgttct 8220
 agttgctttg ttttactggt ttacactggt ctattaggtg ttacatgctg ttcatctggt 8280
 acattgtoga tctgttcatg gtgaacagct ttaaatgcac caaaaactcg taaaagctct 8340
 gatgtatota tcttttttac accgttttca tctgtgcata tggacagttt tccctttgat 8400
 atctaaccgt gaacagttgt tctactttg tttgttagtc ttgatgcttc actgatagat 8460
 acaagagcca taagaacctc agatccttcc gtatttagcc agtatgttct ctagtgtggt 8520
 tcgttggttt tgcgtgagcc atgagaacga accattgaga tcatgcttac tttgcattgc 8580
 actcaaaaaa tttgcctcaa aactggtgag ctgaattttt gcagttaaag catcgtgtag 8640
 tgtttttctt agtccgttac gtaggtagga atctgatga atggtgtgtg gtattttgct 8700
 accattcatt tttatctggt tgttctcaag ttcggttacg agatccattt gtctatctag 8760
 ttcaacttgg aaaaatcaacg tatcagtcgg gcggcctcgc ttatcaacca ccaatttcat 8820
 attgctgtaa gtgtttaaat ctttacttat tggtttcaaa acccattggt taagcctttt 8880
 aaactcatgg tagttatttt caagcattaa catgaactta aattcatcaa ggctaattct 8940
 tatatttggc ttgtgagttt tcttttgtgt tagttctttt aataaccact cataaattct 9000
 catagagtat ttgttttcaa aagacttaac atgttccaga ttatatttta tgaatttttt 9060
 taactggaaa agataaggca atactctctc actaaaaact aattctaatt tttcgttga 9120
 gaacttggca tagtttgtcc actggaaaat ctcaaagcct ttaaccaaag gattcctgat 9180
 ttccacagtt ctgcgtatca gctctctggt tgcttttagct aatacaccat aagcattttc 9240
 cctactgatg ttcacatctt gagcgtattg gttataagtg aacgataaccg tccgttcttt 9300

THE UNIVERSITY OF CHICAGO

<210> 12
<211> 42
<212> DNA

<213> Artificial Sequence

<220>

<223> ribosome binding site

<400> 12

gaaatcatat aactatacct tgattagggg gaccaagaaa tg

42

<210> 13

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> ribosome binding site

<400> 13

caagaacgcg gctggttaaga acataggagc gctgctgaca tg

42

<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> ribosome binding site

<400> 14

tctagaaagg aggtga

16

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> ribosome binding site

<400> 15

tctagaagga ggagaaaaca tg

22

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> ribosome binding site

<400> 16

tctagaggag gagaaaacat g

21

<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> ribosome binding site

<400> 17

20050201 18:03:29

taagaacaaa ggaggagagc tgacatg

27

<210> 18

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> ribosome binding site

<400> 18

taagaacaga ggaggagagc tgacatg

27

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> ribosome binding site

<400> 19

taagaagaaa ggaggtgagc tgacatg

27

206250"BT989209

EMBL-EBI

All Databases

Reset
Advanced[Help Index](#)[General Help](#)[Formats](#)[Gaps](#)[Matrix](#)[References](#)[EMBOSS-Transeq Help](#)[Emboss Programmatic
Access](#)[EBI](#) [Tools](#) [Sequence Analysis](#) [EMBOSS](#)**EMBOSS Transeq**

Transeq translates nucleic acid sequences to the corresponding peptide sequence. It can translate 3 forward or three reverse sense frames, or in all three forward or reverse frames, or in all six frames.

Frame

1 ☐

Regions

START-END

Table

Standard Code

Trim

No ☐

Reverse

No ☐

Color

No ☐

Enter or Paste a nucleic acid Sequence in any format:

```

atggctgaat tactgttagg cgtcaacatt gaccatatcg ctacgctgcg caacgcg
ggtaccgctt acccgatcc ggtgcaggcc gcgtttattg ccgagcaggc gggagcg
ggcattaccg tgcatttacg tgaagatcgc cgtcacatta ctgaccgca cgtgcgc
ctgcgtcaga cgctggatac ccgcatgaat ctggagatgg cggtgaccga agagatg
gcgatcgccg ttgagacgaa gccacatttt tgctgcctgg taccggaaaa gcgtcag
gtaacaaccg aaggcggcct ggatgtcgca gggcagcgtg acaaaatgcg cgatgcc
aaacgtctgg cagatgccgg gattcaggtt tctctgttta ttgacgccga tgaagag
atcaaagctg cggcagaggt tggcgcaccg tttatcgaga tccacaccgg ttgctat
gatgccaaaa ctgacgccga acaggcgcaa gagctggcgc gtatcgccaa agccgcg
tttgccgcaa gcctcgggtc gaaagttaac gccggacacg gtctgacctc tcacaac

```

Upload a file:

If you plan to use these services during a course please [contact us](#).

[Terms of Use](#) : [EBI Funding](#) : [Contact EBI](#) : © European Bioinformatics Institute 2006-2009. EBI is an Outstation of the [European Molecular Biology Laboratory](#)

[Help](#)[General Help](#)[Formats](#)[Gaps](#)[Matrix](#)[References](#)[EMBOSS-Transeq Help](#)**EMBOSS Transeq Results**

Transeq Results	
Frame	1
Translation table	Standard (0)
Regions	START-END
Trim	no
Reverse	no
Color	no
Transeq output	transeq-20090202-16070285811681.output
<input type="button" value="SUBMIT ANOTHER JOB"/>	


>EMBOSS_001_1

```
MAELLG V N I D H I A T L R N A R G T A Y P D P V Q A A F I A E Q A G A D G I T V H L R E D R R H I T D R D V R I
L R Q T L D T R M N L E M A V T E E M L A I A V E T K P H F C C L V P E K R Q E V T T E G G L D V A G Q R D K M R D A C
K R L A D A G I Q V S L F I D A D E E Q I K A A E V G A P F I E I H T G C Y A D A K T D A E Q A Q E L A R I A K A A T
F A A S L G L K V N A G H G L T Y H N V K A I A A I P E M H E L N I G H A I I G R A V M T G L K D A V A E M K R L M L E
A R G *
```

BLAST Basic Local Alignment Search Tool

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Protein Sequence (243 letters)

Results for: lcl|79748 None(243aa) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|79748

Description

None

Molecule type

amino acid

Query Length

243

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Distance tree of results\]](#) [\[Related Structures\]](#)

Search Parameters

Program	blastp
Word size	3
Expect value	10
Hittlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Feb 1, 2009 5:55 PM
Number of letters	2,685,767,600
Number of sequences	7,788,834

Entrez query none

Karlin-Altschul statistics

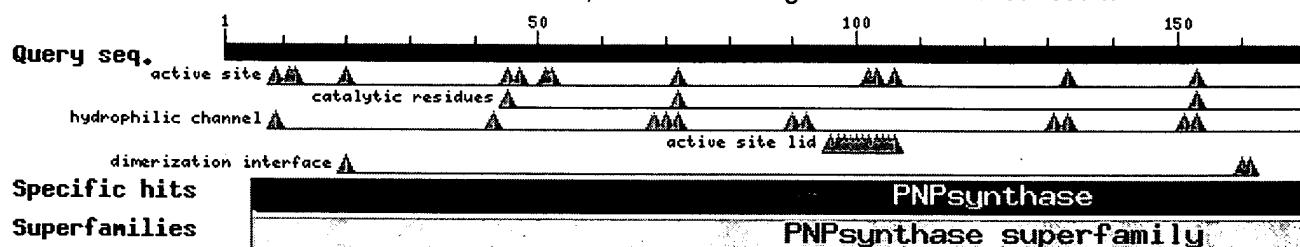
Params	Ungapped	Gapped
Lambda	0.320198	0.267
K	0.133588	0.041
H	0.375908	0.14

Results Statistics

Length adjustment	131
Effective length of query	112
Effective length of database	1665430346
Effective search space	186528198752
Effective search space used	186528198752

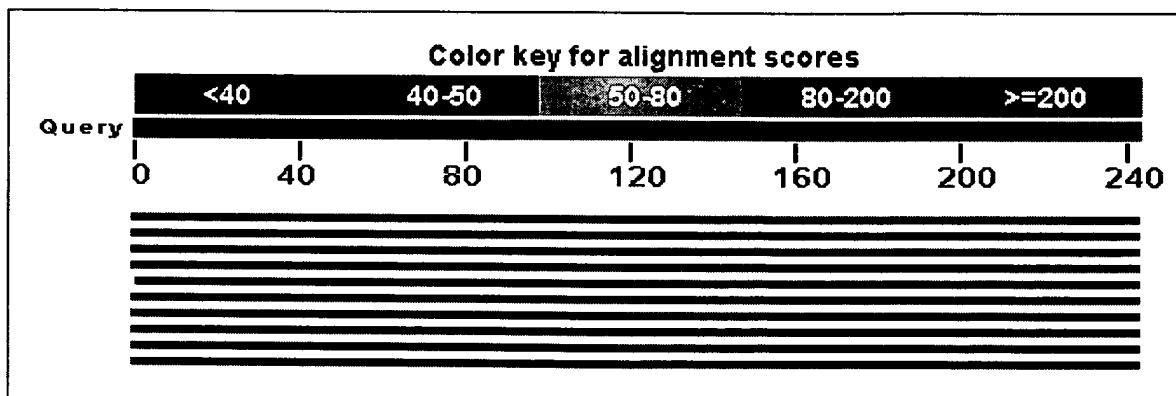
Graphic SummaryShow Conserved Domains

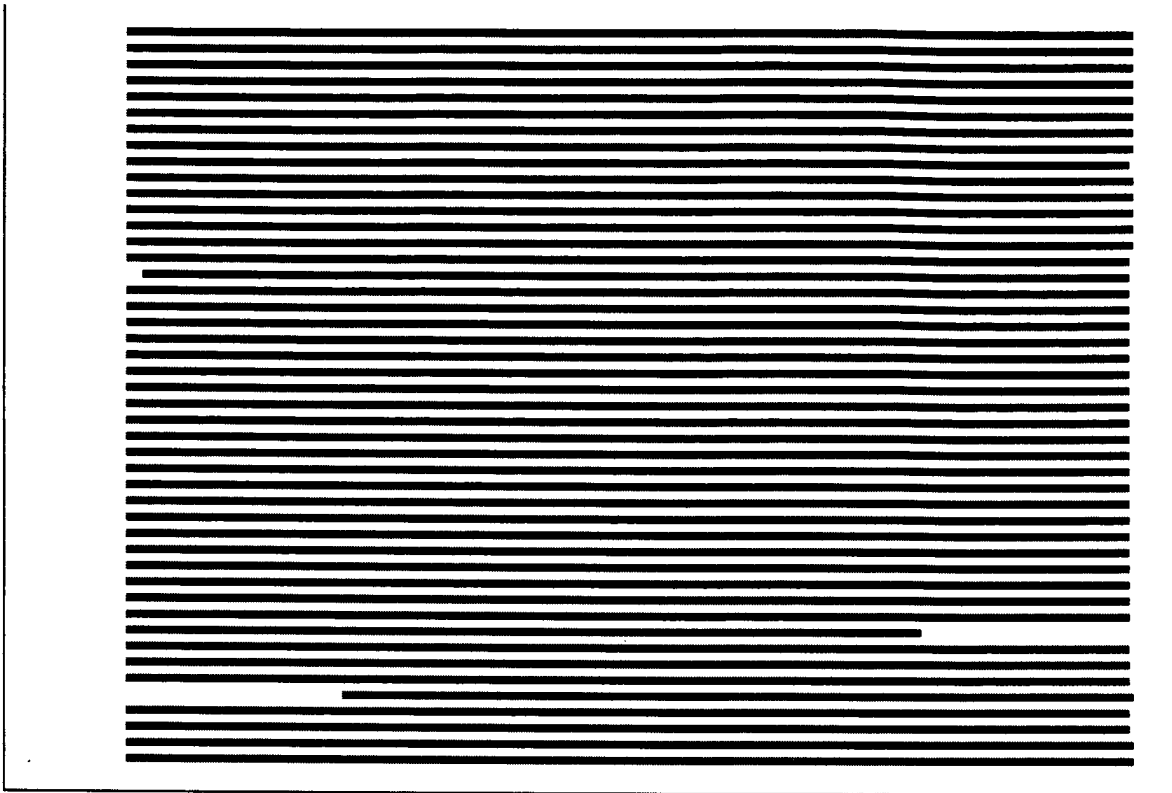
Putative conserved domains have been detected, click on the image below for detailed results.

**Distribution of 100 Blast Hits on the Query Sequence**

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





Descriptions

		Score	
E		(Bits)	Value
Sequences producing significant alignments:			
ref NP_311457.1	pyridoxal phosphate biosynthetic protein Pdx...	491	3e-137
ref YP_002330339.1	pyridoxine 5'-phosphate synthase [Escheri...	489	6e-137
ref NP_289121.1	pyridoxal phosphate biosynthetic protein Pdx...	489	1e-136
ref YP_404339.1	pyridoxal phosphate biosynthetic protein Pdx...	488	1e-136
pdb 1HQ1 A	Chain A, Crystal Structure Of Pyridoxine 5'-Phosph...	488	1e-136
ref YP_001744753.1	pyridoxine 5'-phosphate synthase [Escheri...	488	2e-136
ref YP_403963.1	pyridoxal phosphate biosynthetic protein Pdx...	486	6e-136
ref NP_838137.1	pyridoxal phosphate biosynthetic protein Pdx...	486	6e-136
ref YP_311545.1	pyridoxal phosphate biosynthetic protein Pdx...	486	9e-136
ref ZP_02902009.1	pyridoxine 5'-phosphate synthase [Escheric...	485	1e-135
ref YP_541876.1	pyridoxal phosphate biosynthetic protein Pdx...	484	3e-135
gb ABK20147.1	pyridoxal phosphate biosynthetic protein [Shig...	483	4e-135
ref YP_670456.1	pyridoxal phosphate biosynthetic protein Pdx...	483	5e-135
ref NP_754969.1	pyridoxal phosphate biosynthetic protein Pdx...	482	1e-134
sp Q8FF18.3 PDXJ	ECOL6 RecName: Full=Pyridoxine 5'-phosphate ...	482	1e-134
ref YP_001451819.1	pyridoxal phosphate biosynthetic protein ...	480	5e-134
ref YP_001336529.1	pyridoxal phosphate biosynthetic protein ...	462	1e-128
ref YP_002237093.1	pyridoxine 5'-phosphate synthase [Klebsie...	462	1e-128
ref ZP_03283638.1	hypothetical protein ENTCAN_03445 [Enterob...	461	2e-128
ref NP_457107.1	pyridoxal phosphate biosynthetic protein Pdx...	461	3e-128
ref NP_461513.1	pyridoxal phosphate biosynthetic protein Pdx...	460	4e-128
ref YP_149621.1	pyridoxal phosphate biosynthetic protein Pdx...	460	4e-128
ref YP_001569382.1	pyridoxal phosphate biosynthetic protein ...	459	1e-127
ref YP_002147536.1	pyridoxine 5'-phosphate synthase [Salmone...	458	2e-127
ref YP_001177766.1	pyridoxal phosphate biosynthetic protein ...	451	3e-125
ref ZP_03086581.1	pyridoxal phosphate biosynthetic protein P...	451	3e-125
ref YP_001436809.1	pyridoxal phosphate biosynthetic protein ...	437	3e-121
ref ZP_00822617.1	COG0854: Pyridoxal phosphate biosynthesis ...	397	4e-109
ref ZP_00830259.1	COG0854: Pyridoxal phosphate biosynthesis ...	394	3e-108
ref YP_001005353.1	pyridoxal phosphate biosynthetic protein ...	393	5e-108
ref YP_001400120.1	pyridoxal phosphate biosynthetic protein ...	392	2e-107
ref NP_668623.1	pyridoxal phosphate biosynthetic protein Pdx...	391	2e-107
pdb 3F4N A	Chain A, Crystal Structure Of Pyridoxal Phosphate ...	391	3e-107
ref ZP_00833834.1	COG0854: Pyridoxal phosphate biosynthesis ...	390	4e-107
ref ZP_00827187.1	COG0854: Pyridoxal phosphate biosynthesis ...	390	4e-107
ref YP_071394.1	pyridoxal phosphate biosynthetic protein Pdx...	390	4e-107
ref YP_051364.1	pyridoxal phosphate biosynthetic protein Pdx...	390	7e-107
ref YP_001479890.1	pyridoxal phosphate biosynthetic protein ...	382	1e-104
ref YP_455464.1	pyridoxal phosphate biosynthetic protein Pdx...	381	3e-104
ref NP_930557.1	pyridoxal phosphate biosynthetic protein Pdx...	376	7e-103
ref YP_855346.1	pyridoxal phosphate biosynthetic protein Pdx...	376	9e-103
ref ZP_03318787.1	hypothetical protein PROVALCAL_01725 [Prov...	373	7e-102
ref ZP_02961267.1	hypothetical protein PROSTU_03281 [Provide...	373	7e-102
ref YP_002151612.1	pyridoxal phosphate biosynthetic protein ...	372	1e-101
ref YP_001143199.1	pyridoxal phosphate biosynthetic protein ...	372	2e-101
ref ZP_03315319.1	hypothetical protein PROVRUST_02121 [Provi...	367	4e-100

ref ZP_01262022.1	pyridoxal phosphate biosynthetic protein [...	361	3e-98
ref ZP_03385196.1	pyridoxal phosphate biosynthetic protein P...	360	4e-98
ref YP_205467.1	pyridoxal phosphate biosynthetic protein Pdx...	360	5e-98
ref YP_002073491.1	pyridoxal phosphate biosynthetic protein ...	358	1e-97
ref YP_002156883.1	pyridoxal phosphate biosynthetic protein ...	358	2e-97
ref ZP_03400922.1	pyridoxal phosphate biosynthetic protein P...	357	5e-97
ref NP_760465.1	pyridoxal phosphate biosynthetic protein Pdx...	356	9e-97
ref YP_131204.1	pyridoxal phosphate biosynthetic protein Pdx...	355	1e-96
ref ZP_01816562.1	pyridoxal phosphate biosynthetic protein P...	354	3e-96
ref YP_001906938.1	Pyridoxal phosphate biosynthetic protein ...	354	4e-96
ref ZP_01161526.1	pyridoxal phosphate biosynthetic protein [...	353	7e-96
ref YP_002127690.1	pyridoxal phosphate biosynthetic protein ...	353	1e-95
ref ZP_01870295.1	pyridoxal phosphate biosynthetic protein P...	352	1e-95
ref YP_588729.1	pyridoxal phosphate biosynthetic protein Pdx...	352	1e-95
ref ZP_01220096.1	pyridoxal phosphate biosynthetic protein [...	352	2e-95
ref YP_002263870.1	pyridoxal phosphate biosynthetic protein ...	352	2e-95
ref ZP_01236135.1	pyridoxal phosphate biosynthetic protein [...	352	2e-95
gb EED26525.1	pyridoxal phosphate biosynthetic protein PdxJ ...	351	2e-95
ref ZP_01988133.1	pyridoxal phosphate biosynthetic protein P...	350	4e-95
ref ZP_01215567.1	pyridoxal phosphate biosynthetic protein [...	350	5e-95
ref ZP_01064680.1	pyridoxal phosphate biosynthetic protein [...	349	1e-94
gb EAAZ49556.1	pyridoxal phosphate biosynthetic protein PdxJ ...	348	2e-94
ref NP_798948.1	pyridoxal phosphate biosynthetic protein Pdx...	348	3e-94
ref ZP_00991369.1	pyridoxal phosphate biosynthetic protein [...	347	4e-94
ref NP_232087.1	pyridoxal phosphate biosynthetic protein Pdx...	347	5e-94
ref ZP_02196848.1	pyridoxal phosphate biosynthetic protein P...	347	6e-94
ref ZP_01681976.1	pyridoxal phosphate biosynthetic protein P...	347	7e-94
ref ZP_01949430.1	pyridoxal phosphate biosynthetic protein P...	345	1e-93
ref YP_663265.1	pyridoxal phosphate biosynthetic protein Pdx...	345	2e-93
ref ZP_03354955.1	pyridoxal phosphate biosynthetic protein P...	343	6e-93
ref ZP_01898798.1	pyridoxal phosphate biosynthetic protein [...	343	7e-93
ref ZP_03347562.1	pyridoxal phosphate biosynthetic protein P...	340	6e-92
ref ZP_01614216.1	pyridoxal phosphate biosynthetic protein [...	339	1e-91
ref ZP_01450587.1	pyridoxal phosphate biosynthetic protein [...	338	3e-91
ref YP_563765.1	pyridoxal phosphate biosynthetic protein Pdx...	335	1e-90
ref YP_001553716.1	pyridoxal phosphate biosynthetic protein ...	335	2e-90
ref YP_270774.1	pyridoxal phosphate biosynthetic protein Pdx...	335	2e-90
ref YP_734973.1	pyridoxal phosphate biosynthetic protein Pdx...	335	3e-90
ref YP_339261.1	pyridoxal phosphate biosynthetic protein Pdx...	334	4e-90
ref YP_002359017.1	pyridoxal phosphate biosynthetic protein ...	334	4e-90
ref YP_001365462.1	pyridoxal phosphate biosynthetic protein ...	334	4e-90
ref YP_001182689.1	pyridoxal phosphate biosynthetic protein ...	333	8e-90
ref YP_001049591.1	pyridoxal phosphate biosynthetic protein ...	333	8e-90
ref YP_001500902.1	pyridoxal phosphate biosynthetic protein ...	332	1e-89
ref YP_733968.1	pyridoxal phosphate biosynthetic protein Pdx...	332	2e-89
ref YP_751604.1	pyridoxal phosphate biosynthetic protein Pdx...	332	2e-89
ref YP_964373.1	pyridoxal phosphate biosynthetic protein Pdx...	332	2e-89
ref YP_001673314.1	pyridoxal phosphate biosynthetic protein ...	330	7e-89
ref YP_001093187.1	pyridoxal phosphate biosynthetic protein ...	329	1e-88
ref YP_001759633.1	pyridoxal phosphate biosynthetic protein ...	329	1e-88
ref YP_870654.1	pyridoxal phosphate biosynthetic protein Pdx...	329	1e-88
ref NP_716971.1	pyridoxal phosphate biosynthetic protein Pdx...	328	2e-88
ref YP_942095.1	pyridoxal phosphate biosynthetic protein Pdx...	326	3e-88

ref|YP_693348.1| pyridoxal phosphate biosynthetic protein Pdx... 328 3e-88

[Alignments](#) [Select All](#) [Get selected sequences](#) [Distance tree of results](#)

>ref|NP_311457.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c
O157:H7 str. Sakai]

ref|NP_417059.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12
substr. MG1655]

ref|AP_003150.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12
substr. W3110]

71 more sequence titles

ref|YP_001463887.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia
E24377A]

ref|YP_001459361.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichi
HS]

ref|ZP_02773388.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4113]

ref|ZP_02782782.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4401]

ref|ZP_02786192.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4501]

ref|ZP_02793675.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4486]

ref|ZP_02798517.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4196]

ref|ZP_02803548.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4076]

ref|ZP_02812931.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC869]

ref|ZP_02823953.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC508]

ref|YP_001724107.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichi
ATCC 8739]

ref|YP_001731493.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K
DH10B]

ref|ZP_03002699.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c
53638]

ref|ZP_03029794.1| pyridoxine 5'-phosphate synthase [Escherichia coli B7A]

ref|ZP_03045127.1| pyridoxine 5'-phosphate synthase [Escherichia coli E22]

ref|ZP_03049293.1| pyridoxine 5'-phosphate synthase [Escherichia coli E110019]

ref|ZP_03061820.1| pyridoxine 5'-phosphate synthase [Escherichia coli B171]

ref|ZP_03069709.1| pyridoxine 5'-phosphate synthase [Escherichia coli 101-1]

ref|ZP_03082093.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c
O157:H7 str. EC4024]

ref|ZP_03251256.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4206]

ref|ZP_03255815.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4045]

ref|ZP_03259661.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
EC4042]

ref|YP_002272039.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O157:H
EC4115]

ref|YP_002294127.1| **G** pyridoxal phosphate biosynthetic protein [Escherichia col

ref|ZP_03442750.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 s
TW14588]

ref|YP_002381699.1| **G** pyridoxine 5'-phosphate synthase [Escherichia fergusonii
35469]

ref|YP_002388058.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli IAI1]

ref|YP_002403859.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli 55989]

sp|P0A794.2|PDXJ_ECOLI RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

sp|P0A795.2|PDXJ_ECO57 RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

pdb|1M5W|A **S** Chain A, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate

Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate

pdb|1M5W|B **S** Chain B, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate

Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate

pdb|1M5W|C **S** Chain C, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|D **S** Chain D, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|E **S** Chain E, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|F **S** Chain F, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|G **S** Chain G, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
pdb|1M5W|H **S** Chain H, 1.96 A Crystal Structure Of Pyridoxine 5'-Phosphate Synthase In Complex With 1-Deoxy-D-Xylulose Phosphate
gb|AAA24315.1| pdxJ
gb|AAA21845.1| pdxJ
gb|AAA79826.1| CG Site No. 416
gb|AAC75617.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K-12 substr. MG1655]
dbj|BAB36853.1| **G** pyridoxine biosynthesis [Escherichia coli O157:H7 str. Sakai]
dbj|BAE76740.1| pyridoxine 5'-phosphate synthase [Escherichia coli str. K12 sub W3110]
gb|ABV06978.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli HS]
gb|ABV20635.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli E24377A]
gb|ACA76780.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli ATCC 8739]
gb|ACB03715.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli str. K12 su DH10B]
gb|EDU34578.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4196]
gb|EDU55194.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4113]
gb|EDU65731.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 53638]
gb|EDU72247.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4076]
gb|EDU73719.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4401]
gb|EDU80638.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4486]
gb|EDU86799.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4501]
gb|EDU90661.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC869]
gb|EDU97102.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC508]
gb|EDV61746.1| pyridoxine 5'-phosphate synthase [Escherichia coli B7A]
gb|EDV82886.1| pyridoxine 5'-phosphate synthase [Escherichia coli E22]
gb|EDV88722.1| pyridoxine 5'-phosphate synthase [Escherichia coli E110019]
gb|EDX28996.1| pyridoxine 5'-phosphate synthase [Escherichia coli B171]
gb|EDX39410.1| pyridoxine 5'-phosphate synthase [Escherichia coli 101-1]
gb|EDZ78321.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4206]
gb|EDZ84450.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4045]
gb|EDZ87146.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. EC4042]
gb|ACI35060.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str EC4115]
dbj|BAG78376.1| **G** pyridoxal phosphate biosynthetic protein [Escherichia coli SE
gb|EEC27459.1| pyridoxine 5'-phosphate synthase [Escherichia coli O157:H7 str. TW14588]
emb|CAU98723.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
emb|CAQ88058.1| **G** pyridoxine 5'-phosphate synthase [Escherichia fergusonii]
emb|CAQ99513.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 Length=243

GENE ID: 914900 ECs3430 | pyridoxal phosphate biosynthetic protein PdxJ
 [Escherichia coli O157:H7 str. Sakai] (Over 10 PubMed links)

Score = 491 bits (1263), Expect = 3e-137, Method: Compositional matrix adjust.
Identities = 243/243 (100%), Positives = 243/243 (100%), Gaps = 0/243 (0%)

```
Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGLDVAGQORDKMRDAC 120
Sbjct 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGLDVAGQORDKMRDAC 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241  ARG 243
Sbjct 241  ARG 243
```

>ref|YP_002330339.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O127:H E2348/69]

ref|YP_002413587.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli UMN026
emb|CAS10389.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli O127:H6 st E2348/69]

emb|CAR14061.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
Length=243

GENE ID: 7062394 **pdxJ** | pyridoxine 5'-phosphate synthase
[Escherichia coli O127:H6 E2348/69] (10 or fewer PubMed links)

Score = 489 bits (1260), Expect = 6e-137, Method: Compositional matrix adjust.
Identities = 242/243 (99%), Positives = 243/243 (100%), Gaps = 0/243 (0%)

```
Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGLDVAGQORDKMRDAC 120
Sbjct 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGLDVAGQORDKMRDAC 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121  KRLA+AGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241  ARG 243
Sbjct 241  ARG 243
```

>ref|NP_289121.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c O157:H7 EDL933]

pir||C85902 pyridoxine biosynthesis [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

gb|AAG57679.1|AE005487_3 **G** pyridoxine biosynthesis [Escherichia coli O157:H7 ED Length=243

GENE ID: 957924 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
[Escherichia coli O157:H7 EDL933] (10 or fewer PubMed links)

Score = 489 bits (1258), Expect = 1e-136, Method: Compositional matrix adjust.
Identities = 242/243 (99%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

```
Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
```

```

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
Sbjct 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241  ARG  243
Sbjct 241  ARG  243

```

>ref|YP_404339.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella dysenteriae Sd197]

sp|Q32CV7.1|PDXJ SHIDS **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=gb|ABB62848.1| **G** pyridoxine biosynthesis [Shigella dysenteriae Sd197]
Length=243

GENE ID: 3795506 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Shigella dysenteriae Sd197] (10 or fewer PubMed links)

Score = 488 bits (1257), Expect = 1e-136, Method: Compositional matrix adjust.
Identities = 242/243 (99%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
Sbjct 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
Sbjct 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241  ARG  243
Sbjct 241  ARG  243

```

>pdb|1HO1|A **S** Chain A, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase

pdb|1HO1|B **S** Chain B, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase

pdb|1HO1|C **S** Chain C, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
21 more sequence titles

pdb|1HO1|D **S** Chain D, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase

pdb|1HO4|A **S** Chain A, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate

pdb|1HO4|B **S** Chain B, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate

pdb|1HO4|C **S** Chain C, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate

pdb|1HO4|D **S** Chain D, Crystal Structure Of Pyridoxine 5'-Phosphate Synthase
In Complex With Pyridoxine 5'-Phosphate And Inorganic Phosphate

pdb|1IXN|A **S** Chain A, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXN|B **S** Chain B, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

pdb|1IXN|C **S** Chain C, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase

Synthase

pdb|1IXN|D **S** Chain D, Enzyme-Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXO|A **S** Chain A, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXO|B **S** Chain B, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXO|C **S** Chain C, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXO|D **S** Chain D, Enzyme-Analogue Substrate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXP|A **S** Chain A, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXP|B **S** Chain B, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXP|C **S** Chain C, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXP|D **S** Chain D, Enzyme-Phosphate Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXQ|A **S** Chain A, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXQ|B **S** Chain B, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXQ|C **S** Chain C, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase
pdb|1IXQ|D **S** Chain D, Enzyme-Phosphate2 Complex Of Pyridoxine 5'-Phosphate Synthase
 Length=242

Score = 488 bits (1257), Expect = 1e-136, Method: Compositional matrix adjust.
 Identities = 242/242 (100%), Positives = 242/242 (100%), Gaps = 0/242 (0%)

Query	2	AELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	61
		AELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	
Sbjct	1	AELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	62	RQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQREVTEGGLDVAGQRDKMRDACK	121
		RQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQREVTEGGLDVAGQRDKMRDACK	
Sbjct	61	RQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQREVTEGGLDVAGQRDKMRDACK	120
Query	122	RLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAATF	181
		RLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAATF	
Sbjct	121	RLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAATF	180
Query	182	AASLGLKVNAGHGLTYHNVKAIAAIPMHHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEA	241
		AASLGLKVNAGHGLTYHNVKAIAAIPMHHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEA	
Sbjct	181	AASLGLKVNAGHGLTYHNVKAIAAIPMHHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEA	240
Query	242	RG	243
		RG	
Sbjct	241	RG	242

>ref|YP_001744753.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli SMS-3-
 ref|YP_002408707.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli IAI39]
 gb|ACB18311.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli SMS-3-5]
 emb|CAR18891.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 Length=243

GENE ID: 6143419 **pdxJ** | pyridoxine 5'-phosphate synthase
 [Escherichia coli SMS-3-5]

Score = 488 bits (1256), Expect = 2e-136, Method: Compositional matrix adjust.
 Identities = 241/243 (99%), Positives = 243/243 (100%), Gaps = 0/243 (0%)

Query	1	MAELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		MAELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	
Sbjct	1	MAELLGVLNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60

```


Query   61   LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC   120
Sbjct   61   LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ+KMRDAC   120




Query   121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT   180
Sbjct   121  KRLA+AGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT   180

Query   181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
Sbjct   181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240

Query   241   ARG   243
Sbjct   241   ARG   243

```

>ref|YP_408963.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shigella boyd Sb227]

ref|YP_001881343.1|  pyridoxine 5'-phosphate synthase [Shigella boydii CDC 308 sp|Q31XS3.1|PDXJ SHIBS RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN gb|ABB67135.1|  pyridoxine biosynthesis [Shigella boydii Sb227] gb|ACD10043.1|  pyridoxine 5'-phosphate synthase [Shigella boydii CDC 3083-94] Length=243

GENE ID: 3781575 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Shigella boydii Sb227] (10 or fewer PubMed links)

Score = 486 bits (1252), Expect = 6e-136, Method: Compositional matrix adjust.
Identities = 240/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

```

Query   1   MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI   60
Sbjct   1   MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI   60


Query   61   LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC   120
Sbjct   61   LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ+KMRDAC   120


Query   121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT   180
Sbjct   121  KRLDAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELRIAKAAT   180


Query   181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
Sbjct   181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240


Query   241   ARG   243
Sbjct   241   ARG   243


```


>ref|NP_838137.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shigella flex 2a str. 2457T]

ref|NP_708416.2|  pyridoxal phosphate biosynthetic protein PdxJ [Shigella flex 2a str. 301]

ref|YP_690029.1|  pyridoxal phosphate biosynthetic protein PdxJ [Shigella flex 5 str. 8401]

ref|ZP_03064347.1| pyridoxine 5'-phosphate synthase [Shigella dysenteriae 1012] gb|AAP17947.1|  pyridoxal phosphate biosynthetic protein [Shigella flexneri 2a str. 2457T]

gb|AAN44123.2|  pyridoxal phosphate biosynthetic protein [Shigella flexneri 2a str. 301]

gb|ABF04724.1|  pyridoxine biosynthesis [Shigella flexneri 5 str. 8401]

gb|EDX35667.1| pyridoxine 5'-phosphate synthase [Shigella dysenteriae 1012] Length=243

GENE ID: 1079066 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Shigella flexneri 2a str. 2457T] (10 or fewer PubMed links)

Score = 486 bits (1251), Expect = 6e-136, Method: Compositional matrix adjust.
Identities = 240/243 (98%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

```

Query   1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct   1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query   61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
Sbjct   61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQOR+K+RDAC 120
          LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQREKIRDAC 120

Query   121     KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct   121     KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQEL RIAKAAT 180
          KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELVRIAKAAT 180

Query   181     FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct   181     FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query   241     ARG      243
Sbjct   241     ARG      243

```

>ref|YP_311545.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shigella sonnei Ss046]
 sp|Q3YYV2.1|PDXJ SHISS **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
 gb|AAZ89310.1| **G** pyridoxine biosynthesis [Shigella sonnei Ss046]
 Length=243

GENE ID: 3669253 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
 [Shigella sonnei Ss046] (10 or fewer PubMed links)

Score = 486 bits (1250), Expect = 9e-136, Method: Compositional matrix adjust.
 Identities = 239/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

```

Query   1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct   1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query   61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
Sbjct   61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQOR+KMRDAC 120
          LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQREKMRDAC 120

Query   121     KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct   121     KRLDAGIQ+SLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQEL RIAKAAT 180
          KRLTDAGIQISLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELVRIAKAAT 180

Query   181     FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct   181     FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query   241     ARG      243
Sbjct   241     ARG      243

```

>ref|ZP_02902009.1| pyridoxine 5'-phosphate synthase [Escherichia albertii TW076
 gb|EDS92821.1| pyridoxine 5'-phosphate synthase [Escherichia albertii TW07627]
 Length=243

Score = 485 bits (1249), Expect = 1e-135, Method: Compositional matrix adjust.
 Identities = 240/243 (98%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

```

Query   1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
Sbjct   1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query   61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
Sbjct   61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQOR KMRDAC 120
          LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRGKMRDAC 120

Query   121     KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
Sbjct   121     KRLADAGIQVSLFIDADEEQIKAAA+VGAPFIEIHTGCIYADAKTDAEQAQELARIAKAA+ 180
          KRLADAGIQVSLFIDADEEQIKAAAADVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAS 180

Query   181     FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct   181     FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

```

Query 241 ARG 243
Sbjct 241 ARG 243

>ref|YP_541876.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli UTI89]
ref|YP_853698.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli APEC 01]
gb|ABE08345.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli UTI89]
gb|ABJ01984.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli APEC 01]
Length=248

GENE ID: 3989796 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli UTI89] (10 or fewer PubMed links)

Score = 484 bits (1245), Expect = 3e-135, Method: Compositional matrix adjust.
Identities = 240/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Sbjct	6	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDV I	65
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	66	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	125
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT	180
Sbjct	126	KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT	185
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	186	FATSLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	245
Query	241	ARG	243
Sbjct	246	ARG	248

>gb|ABK20147.1| pyridoxal phosphate biosynthetic protein [Shigella boydii]
Length=243

Score = 483 bits (1244), Expect = 4e-135, Method: Compositional matrix adjust.
Identities = 238/243 (97%), Positives = 239/243 (98%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Sbjct	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADG TVHLREDRRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT	180
Sbjct	121	KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDTVAEMKRLMLE	240
Query	241	ARG	243
Sbjct	241	ARG	243

>ref|YP_670456.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 536]
ref|ZP_03035524.1| pyridoxine 5'-phosphate synthase [Escherichia coli F11]
ref|YP_002392398.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli S88]
7 more sequence titles

ref|YP_002398892.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli ED1a]
 ref|YP_002557403.1| **G** Pyridoxine 5'-phosphate synthase [Escherichia coli LF82]
 gb|ABG70555.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 536]
 gb|EDV65320.1| pyridoxine 5'-phosphate synthase [Escherichia coli F11]
 emb|CAR04001.1| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 emb|CAR09161.2| **G** pyridoxine 5'-phosphate synthase [Escherichia coli]
 emb|CAP77010.1| **G** Pyridoxine 5'-phosphate synthase [Escherichia coli LF82]
 Length=243

GENE ID: 4190772 ECP 2566 | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli 536] (10 or fewer PubMed links)

Score = 483 bits (1244), Expect = 5e-135, Method: Compositional matrix adjust.
 Identities = 240/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	FATSLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>ref|NP_754969.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli CFT073]

gb|AAN81537.1|AE016764_219 **G** Pyridoxal phosphate biosynthetic protein pdxJ [Escherichia coli CFT073]
 Length=248

GENE ID: 1038793 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Escherichia coli CFT073] (10 or fewer PubMed links)


Score = 482 bits (1241), Expect = 1e-134, Method: Compositional matrix adjust.
 Identities = 239/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)


Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	6	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVI	65
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	66	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	125
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	126	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	185
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	186	FATSLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	245
Query	241	ARG 243	
Sbjct	246	ARG 248	

>sp|Q8FF18.3|PDXJ_ECOL6 RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 Length=243

Score = 482 bits (1240), Expect = 1e-134, Method: Compositional matrix adjust.
Identities = 239/243 (98%), Positives = 241/243 (99%), Gaps = 0/243 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDV I	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	


>ref|YP_001451819.1|  pyridoxal phosphate biosynthetic protein PdxJ [Citrobacte ATCC BAA-895]


gb|ABV11383.1|  hypothetical protein CKO_00218 [Citrobacter koseri ATCC BAA-89 Length=243]

GENE ID: 5585068 CKO_00218 | pyridoxal phosphate biosynthetic protein PdxJ
[Citrobacter koseri ATCC BAA-895]

Score = 480 bits (1235), Expect = 5e-134, Method: Compositional matrix adjust.
Identities = 236/243 (97%), Positives = 242/243 (99%), Gaps = 0/243 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	KRLADAGI VSLFIDADEEQIKAAA+VGAP+IEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	FAASLGLKVNAGHGLTYHNV+AI AAIPEMHENLIGHAIIGRAVM+GLK+AVAEMKRLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>ref|YP_001336529.1|  pyridoxal phosphate biosynthetic protein PdxJ [Klebsiella subsp. pneumoniae MGH 78578]

gb|ABR78299.1|  pyridoxal phosphate biosynthetic protein [Klebsiella pneumonia subsp. pneumoniae MGH 78578]
Length=243

GENE ID: 5342763 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Klebsiella pneumoniae subsp. pneumoniae MGH 78578]

Score = 462 bits (1188), Expect = 1e-128, Method: Compositional matrix adjust.
Identities = 228/243 (93%), Positives = 236/243 (97%), Gaps = 0/243 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	61	LRQTL TRMNLEMAVTEEML IA ETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180

```

Sbjct 121 +RLADAGI VSLFIDADE QIKAAA+VGAP+IEIHTGCIYADAKTDAEQQA+EL RIAKAAT 180
          QRLADAGILVSLFIDADEAQIKAAAADV GAPIEIEHTGCIYADAKTDAEQARELERIAKAAT
Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVM+GLK+AVAEMK LMLE
Sbjct 181 YAASLGLKVNAGHGLTYHNVKAI AALPEMHENLIGHAIIGRAVMSGLKEAVAEMKRLMLE 240
Query 241 ARG 243
          ARG
Sbjct 241 ARG 243

```

>ref|YP_002237093.1| **G** pyridoxine 5'-phosphate synthase [Klebsiella pneumoniae 3
 gb|ACI11352.1| **G** pyridoxine 5'-phosphate synthase [Klebsiella pneumoniae 342]
 Length=243

GENE ID: 6934996 pdxJ | pyridoxine 5'-phosphate synthase
 [Klebsiella pneumoniae 342] (10 or fewer PubMed links)

Score = 462 bits (1188), Expect = 1e-128, Method: Compositional matrix adjust.
 Identities = 227/243 (93%), Positives = 236/243 (97%), Gaps = 0/243 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
          MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTT EGGGLDVAGQRD KMRDAC 120
          LR+TL TRMNLEMAVTEEML IA ETKPHFCCLVPEKRQEVTT EGGGLDVAGQRD KMRDAC
Sbjct 61 LRET LHTRMNLEMAVTEEMLT IACETKPHFCCLVPEKRQEVTT EGGGLDVAGQRD KMRDAC 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGCIYADAKTDAEQQAQELARI AKAAT 180
          +RLADAGI VSLFIDAD EQIKAAA+VGAP+IEIHTGCIYADAKTDA QA+EL RIAKAAT
Sbjct 121 QRLADAGILVSLFIDADNEQIKAAA ADVGAPIEIEHTGCIYADAKTDAGQAKELERIAKAAT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVM+GLK+AVAEMKRLMLE
Sbjct 181 YAASLGLKVNAGHGLTYHNVKAI AALPEMHENLIGHAIIGRAVMSGLKEAVAEMKRLMLE 240
Query 241 ARG 243
          ARG
Sbjct 241 ARG 243

```

>ref|ZP_03283638.1| hypothetical protein ENTCAN_03445 [Enterobacter cancerogenus
 ATCC 35316]
 gb|EEA13217.1| hypothetical protein ENTCAN_03445 [Enterobacter cancerogenus
 ATCC 35316]
 Length=243

Score = 461 bits (1187), Expect = 2e-128, Method: Compositional matrix adjust.
 Identities = 227/242 (93%), Positives = 235/242 (97%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
          MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTT EGGGLDVAGQRD KMRDAC 120
          LRQTL DTRMNLEMAVTEEMLAIA ETKPHFCCLVPEKRQEVTT EGGGLDVAGQ +KMRDAC
Sbjct 61 LRQTL DTRMNLEMAVTEEMLAIA IACETKPHFCCLVPEKRQEVTT EGGGLDVAGQPEKMRDAC 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGCIYADAKTDAEQQAQELARI AKAAT 180
          KRLADAGI VSLFIDAD+ QIKAAA+ GAP+IEIHTGCIYADAK DAEQA+EL RIAKAAT
Sbjct 121 KRLADAGILVSLFIDADDAQIKAAA ADAGAPIEIEHTGCIYADAKNDAEQAKELERIAKAAT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVM+GLKDAVAEMKRLMLE
Sbjct 181 YAASLGLKVNAGHGLTYHNVKAI AALPEMHENLIGHAIIGRAVMSGLKDAVAEMKRLMLE 240
Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|NP_457107.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en
 subsp. enterica serovar Typhi str. CT18]

ref|NP_804155.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en
 subsp. enterica serovar Typhi str. Ty2]

ref|ZP_03358029.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Typhi str. E02-1180]


7 more sequence titles


ref|ZP_03364950.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Typhi str. E98-0664]

ref|ZP_03370878.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Typhi str. E98-2068]

ref|ZP_03376409.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Typhi str. J185]

sp|Q8Z4K6.2|PDXJ_SALTI RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
pir||AH0828 probable pyridoxal phosphate biosynthetic protein STY2824 [imported
- Salmonella enterica subsp. enterica serovar Typhi
(strain CT18)]


emb|CAD02780.1|  putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Typhi]

gb|AA068004.1|  putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Typhi Ty2]
Length=243

GENE ID: 1249133 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Salmonella enterica subsp. enterica serovar Typhi str. CT18]
(10 or fewer PubMed links)

Score = 461 bits (1185), Expect = 3e-128, Method: Compositional matrix adjust.
Identities = 228/243 (93%), Positives = 234/243 (96%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Sbjct	1	MAELLLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Query	61	LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Sbjct	61	LRQTLHTRM NLEMAVTEEM LAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	RLA AGIQVSLFIDADE QI AAAEVGAFFIEIHTGICYA+A+TDAEQA+ELARIA AAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	AA LGLKVNAGHGLTYHNVKAI AA+PEMHELNIGHAIIGRAVMTGLK+AVAEMKRLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>ref|NP_461513.1|  pyridoxal phosphate biosynthetic protein PdxJ [Salmonella typhimurium str. LT2]

ref|ZP_02343149.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]


ref|ZP_02573805.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701]


26 more sequence titles


ref|ZP_02663381.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]

ref|ZP_02668300.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486]


ref|ZP_02683344.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]

ref|YP_002041841.1|  pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL254]

ref|YP_002046640.1|  pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]

ref|YP_002115641.1|  pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633]

ref|ZP_03165472.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23]

ref|YP_002216645.1|  pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]

ref|ZP_03220482.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Javiana str. GA MM04042433]

ref|YP_002227475.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella subsp. enterica serovar Gallinarum str. 287/91]

ref|YP_002244636.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella subsp. enterica serovar Enteritidis str. P125109]

sp|Q8ZN19.2|PDXJ SALTY RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

gb|AAL21472.1| **G** carries out condensation and ring closure step after PdxA in pyridoxine biosynthesis [Salmonella typhimurium LT2]

gb|ACF64860.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL254]

gb|ACF66310.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL476]

gb|ACF91091.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. CVM19633]

gb|EDY26273.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA23]

gb|EDY28219.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Schwarzengrund str. SL480]

gb|ACH75352.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Dublin str. CT_02021853]

gb|EDZ06327.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Javiana str. GA_MM04042433]

emb|CAR38432.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella ent subsp. enterica serovar Gallinarum str. 287/91]

gb|EDZ13051.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Saintpaul str. SARA29]

gb|EDZ15860.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar 4,[5],12:i:- str. CVM23701]

gb|EDZ24330.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Heidelberg str. SL486]

gb|EDZ36146.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Hadar str. RI_05P066]

emb|CAR34140.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Salmonella ent subsp. enterica serovar Enteritidis str. P125109]

Length=243

GENE ID: 1254100 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella typhimurium LT2] (10 or fewer PubMed links)

Score = 460 bits (1184), Expect = 4e-128, Method: Compositional matrix adjust.
Identities = 228/243 (93%), Positives = 234/243 (96%), Gaps = 0/243 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Sbjct	1	MAELLLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Query	61	LRQTL DTRM NLEM AVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC	120
Sbjct	61	LRQTLHTRM NLEM AVTEEMLAI AVETRPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	RLA AGIQVSLFIDADE QI AAAEVGAFFIEIHTGCIYA+A+TDAEQA+ELARIA AAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHelnIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	AA LGLKVNAGHGLTYHNVKAIAA+PEMHEL NIGHAIIGRAVMTGLK+AVAEMKRLMLE	240
Query	241	ARG	243
Sbjct	241	ARG	243

>ref|YP_149621.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en subsp. enterica serovar Paratyphi A str. ATCC 9150]

ref|YP_217560.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en subsp. enterica serovar Choleraesuis str. SC-B67]

ref|YP_001586617.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella subsp. enterica serovar Paratyphi B str. SPB7]

17 more sequence titles

ref|ZP_02657214.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp.

enterica serovar Kentucky str. CDC 191]
ref|ZP_02700515.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL317]
ref|ZP_02833432.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Weltevreden str. HI_N05-537]
ref|ZP_03075503.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188]
ref|YP_002141117.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]
ref|ZP_03214396.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Virchow str. SL491]
sp|Q57LD3.1|PDXJ_SALCH RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
sp|Q3V7K1.1|PDXJ_SALPA RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
gb|AAV76309.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]
gb|AAX66479.1| **G** carries out condensation and ring closure step after PdxA in pyridoxine biosynthesis [Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67]
gb|ABX65784.1| **G** hypothetical protein SPAB_00348 [Salmonella enterica subsp. enterica serovar Paratyphi B str. SPB7]
gb|EDX44722.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Kentucky str. CVM29188]
gb|EDX49461.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Newport str. SL317]
emb|CAR58387.1| **G** putative pyridoxal phosphate biosynthetic protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. AKU_12601]
gb|EDZ03427.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Virchow str. SL491]
gb|EDZ20478.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Kentucky str. CDC 191]
gb|EDZ28717.1| pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Weltevreden str. HI_N05-537]
Length=243

GENE ID: 3178757 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] (10 or fewer PubMed links)

Score = 460 bits (1184), Expect = 4e-128, Method: Compositional matrix adjust.
Identities = 228/243 (93%), Positives = 234/243 (96%), Gaps = 0/243 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRD KMRDAC	120
Sbjct	61	LRQTLHTRM NLEMAVTEEM LAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQRD KMRDAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAAKAT	180
Sbjct	121	RLA AGIQVSLFIDADE QI AAAEVGAFFIEIHTGCIYA+A+TDAEQA+ELARIA AAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMH ELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	AA LGLKVNAGHGLTYHNVKAIAA+PEMH ELNIGHAIIGRAVMTGLK+AVAEMKRLMLE	240
Query	241	ARG 243	
Sbjct	241	ARG 243	

>ref|YP_001569382.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Salmonella subsp. arizonae serovar 62:z4,z23:--]

gb|ABX20240.1| **G** hypothetical protein SARI_00300 [Salmonella enterica subsp. ar serovar 62:z4,z23:--]
Length=243

GENE ID: 5764319 SARI_00300 | pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica subsp. arizonae serovar 62:z4,z23:--]

Score = 459 bits (1180), Expect = 1e-127, Method: Compositional matrix adjust.
Identities = 225/243 (92%), Positives = 233/243 (95%), Gaps = 0/243 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
-------	---	---	----

```

Sbjct 1 MAELLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHI+DRDVRI 60
MAELLLGVNIDHIATLRNARGTDYDPVQAAAFIAEQAGADGITVHLREDRRHISDRDVRI

Query 61 LRQTL DTRMNLEMAVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
LRQTL TRMNLEMAVTEEMLAI AVET+PHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC

Sbjct 61 LRQTLHTRMNLEMAVTEEMLAI AVETRPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEV GAFPIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
RLA AGIQVSLFIDADE QI AA AEV GAFPIEIHTGCIY+AKTDAEQ++ELARIA AAT

Sbjct 121 SRLAAAGIQVSLFIDADEAQINAAAEV GAFPIEIHTGCIYANAKTDAEQSKELARIASAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAI AA IPEMHEL NIGHAI IGRAVMTGLKDAVAEMKRLMLE 240
A LGLKVNAGHGLTYHNVKAI AA +PEMHEL NIGHAI IGRAVMTGLK+AVAEMKRLMLE

Sbjct 181 LAVRLGLKVNAGHGLTYHNVKAI AALPEMHEL NIGHAI IGRAVMTGLKEAVAEMKRLMLE 240

Query 241 ARG 243
ARG
Sbjct 241 ARG 243

```

>ref|YP_002147536.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica sub enterica serovar Agona str. SL483]

gb|ACH50628.1| **G** pyridoxine 5'-phosphate synthase [Salmonella enterica subsp. enterica serovar Agona str. SL483]
Length=243

GENE ID: 6793014 **pdxJ** | pyridoxine 5'-phosphate synthase
[Salmonella enterica subsp. enterica serovar Agona str. SL483]

Score = 458 bits (1179), Expect = 2e-127, Method: Compositional matrix adjust.
Identities = 227/243 (93%), Positives = 233/243 (95%), Gaps = 0/243 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
MAELLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI

Sbjct 1 MAELLLGVNIDHIATLRNARGTDYDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61 LRQTL DTRMNLEMAVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
LRQTL TRMNLEMAVTE MLAI AVET+PHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC

Sbjct 61 LRQTLHTRMNLEMAVTEAMLA IAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEV GAFPIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
RLA AGIQVSLFIDADE QI AA AEV GAFPIEIHTGCIY+A+TDAEQ+ELARIA AAT

Sbjct 121 ARLAAAGIQVSLFIDADERQINAAAEV GAFPIEIHTGCIYANAETDAEQAKELARIASAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAI AA IPEMHEL NIGHAI IGRAVMTGLKDAVAEMKRLMLE 240
AA LGLKVNAGHGLTYHNVKAI AA +PEMHEL NIGHAI IGRAVMTGLK+AVAEMKRLMLE

Sbjct 181 LAARLGLKVNAGHGLTYHNVKAI AALPEMHEL NIGHAI IGRAVMTGLKEAVAEMKRLMLE 240

Query 241 ARG 243
ARG
Sbjct 241 ARG 243

```

>ref|YP_001177766.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Enterobact 638]

gb|ABP61715.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Enterobacter sp 638]
Length=243

GENE ID: 5111760 **Ent638_3051** | pyridoxal phosphate biosynthetic protein PdxJ
[Enterobacter sp. 638]

Score = 451 bits (1160), Expect = 3e-125, Method: Compositional matrix adjust.
Identities = 222/242 (91%), Positives = 233/242 (96%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDV+I

Sbjct 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVKI 60

Query 61 LRQTL DTRMNLEMAVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
LRQTL DTRMNLEMAVTEEMLAI A ETKPHFCCLVPEKRQEVTTTEGGLDVAGQ+DKMRDAC

Sbjct 61 LRQTL DTRMNLEMAVTEEMLAI ACETKPHFCCLVPEKRQEVTTTEGGLDVAGQQDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEV GAFPIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
KRLADAGI VSLFIDAD +QIKAAA VGAP+IEIHTGCIYADA+ + QA+ELARIAKAAT

Sbjct 121 KRLADAGILVSLFIDADFDQIKAAA AVGAPYIEIHTGCIYADAEDVAQAKELARIAKAAT 180

```

```

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AASLGLKVNAGHGLTYHNVKAI A IP EM ELNIGHAIIGRAVM+GLK+AV+EMKRLMLE
Sbjct 181 YAASLGLKVNAGHGLTYHNVKAI AQ IPEMFELNIGHAIIGRAVMSGLKEAVSEMKRLMLE 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_03086581.1| pyridoxal phosphate biosynthetic protein PdxJ [Escherichia c
O157:H7-str. EC4024]
Length=239

Score = 451 bits (1159), Expect = 3e-125, Method: Compositional matrix adjust.
Identities = 220/238 (92%), Positives = 230/238 (96%), Gaps = 0/238 (0%)

```

Query 5 LLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRILRQT 64
          +LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRILRQT
Sbjct 1 MLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRILRQT 60

Query 65 LDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDACKRLA 124
          LDTRMNLEMAVTEEML IA +TKPHFCCLVPEKRQEVTTTEGGLDVAGQ DKMRDACKRLA
Sbjct 61 LDTRMNLEMAVTEEMLTIACTDKPHFCCLVPEKRQEVTTTEGGLDVAGQLDKMRDACKRLA 120

Query 125 DAGIQVSLFIDADEEQIKAAA+EVGAPFIEIHTGICYADAKTDAEQAQELARIAKAATFAAS 184
          DAGI VSLFIDAD QIKAAA+VGAP+IEIHTGICYADAK DAEQA+EL RIAKAAT+AAS
Sbjct 121 DAGILVSLFIDADFAQIKAAA+DVGAPYIEIHTGICYADAKNDAEQAKELERIAKAATYAAS 180

Query 185 LGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEAR 242
          LGLKVNAGHGLTYHNVKAI AA+PEMHELNIGHAIIGRAVM+GLK+AV+EMKRLMLEAR
Sbjct 181 LGLKVNAGHGLTYHNVKAI AALPEMHELNIGHAIIGRAVMSGLKEAVSEMKRLMLEAR 238

```

>ref|YP_001436809.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Enterobact
ATCC BAA-894]

gb|ABU75973.1| **G** hypothetical protein ESA_00695 [Enterobacter sakazakii ATCC BA
Length=243]

GENE ID: 5551187 ESA_00695 | pyridoxal phosphate biosynthetic protein PdxJ
[Enterobacter sakazakii ATCC BAA-894]

Score = 437 bits (1124), Expect = 3e-121, Method: Compositional matrix adjust.
Identities = 216/242 (89%), Positives = 227/242 (93%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60

Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          LRQTL TRMNLEMAVTEEML IA ETKPHFCCLVPEKRQEVTTTEGGLDVAGQ DKMRDAC
Sbjct 61 LRQTLHTRMNLEMAVTEEMLTIACTKPHFCCLVPEKRQEVTTTEGGLDVAGQLDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAA+EVGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          +RLA AGI VSLFIDAD QI AA VGAP+IEIHTGICYADA+ DA +A+EL RIAKAAT
Sbjct 121 QRLAAAGILVSLFIDADNAQIDA+AVAVGAPYIEIHTGICYADAEDDATRARELERIAKAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AAS GLKVNAGHGLTYHNV+AIAA+PEMHELNIGHAIIGRAVM+GLK+AV+EMKRLMLE
Sbjct 181 YAASKGLKVNAGHGLTYHNVQAIAALPEMHELNIGHAIIGRAVMSGLKEAVSEMKRLMLE 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_00822617.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia
ATCC 43970]
Length=243

Score = 397 bits (1020), Expect = 4e-109, Method: Compositional matrix adjust.
Identities = 198/242 (81%), Positives = 212/242 (87%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI
Sbjct 1 MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60

Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A

```



```

Sbjct 61 LRQTIQTRMNLEMAVTDEMVGIACELQPHFCCLVPEKRQEVTTTEGGLDVAGQIDKMTVAV 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RLA+AGI VSLFIDAD QI AA VGAP+IEIHTG YADA TD + EL RI KAAT
Sbjct 121 SRLAEAGILVSLFIDADMRQIDAAVTVGAPYIEIHTGAYADATTDLARQELVRITKAAT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AAS GLKVNAGHGLTYHNV+ IAA+PE+HELNIGHAIIG+AVMTGL AV+EMK LM E
Sbjct 181 YAASKGLKVNAGHGLTYHNVQPIAALPEIHELNIGHAIIGQAVMTGLAAAVSEMKVLMRE 240
Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_00830259.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 33641]
Length=243

Score = 394 bits (1013), Expect = 3e-108, Method: Compositional matrix adjust.
Identities = 196/242 (80%), Positives = 211/242 (87%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
          MA+LLLGVNIDHIATLRNARGT YPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI
Sbjct 1 MADLLLGVNIDHIATLRNARGTIYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A
Sbjct 61 LRQTIQTRMNLEMAVTDEMVDIACELQPHFCCLVPEKRQEVTTTEGGLDVAGQIDKMTIAV 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RL++AGI VSLFIDAD QI AA VGAP+IEIHTG YADA +D + EL RIAKAAT
Sbjct 121 SRLSEAGILVSLFIDADMRQIDAAVTVGAPYIEIHTGAYADATSDLARQELVRIAKAAT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVM+GL AV EMK LM E
Sbjct 181 YAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMSGLATAVTEMKVLMRE 240
Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|YP_001005353.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia e subsp. enterocolitica 8081]

emb|CAL11118.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia enter subsp. enterocolitica 8081]
Length=243

GENE ID: 4716617 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
[Yersinia enterocolitica subsp. enterocolitica 8081] (10 or fewer PubMed links)

Score = 393 bits (1010), Expect = 5e-108, Method: Compositional matrix adjust.
Identities = 196/242 (80%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
          MA+LLLGVNIDHIATLRNARGT YPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI
Sbjct 1 MADLLLGVNIDHIATLRNARGTIYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          LR+T+ TRMNLEMAVT+EM+ IA E PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A
Sbjct 61 LRETIQTRMNLEMAVTDEMVGIACEINPHFCCLVPEKRQEVTTTEGGLDVAGQIDKMTVAV 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RLA AGI VSLFIDAD QI AA VGAP+IEIHTG YADA +D + EL RIAKAAT
Sbjct 121 SRLAKAGILVSLFIDADMRQIDAAVAVGAPYIEIHTGAYADATSDLARQELVRIAKAAT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AAS GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVM+GL AV +MK LM E
Sbjct 181 YAASKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMSGLAAAVTDMKVLMRE 240
Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|YP_001400120.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p

IP 31758]

gb|ABS47286.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudo
IP 31758]
Length=243

GENE ID: 5386119 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Yersinia pseudotuberculosis IP 31758] (10 or fewer PubMed links)

Score = 392 bits (1006), Expect = 2e-107, Method: Compositional matrix adjust.
Identities = 197/242 (81%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

```

Query   1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI   60
Sbjct   1      MA+LLLGVNIDHIATLRNARGT YDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI   60
Query   61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC   120
Sbjct   61      LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTTTEGGLDVAGQ DKM  A   120
Query   121     KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT   180
Sbjct   121     RLAD GI VSLFIDAD QI AA .GAP+IEIHTG YADA T E+ EL RIAKAAT   180
Query   181     FAASLGLKVNAGHGLTYHNVKAIATAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
Sbjct   181     +AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E   240
Query   241     AR   242
Sbjct   241     AR   242

```

>**ref|NP_668623.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
KIM]

ref|NP_993846.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Microtus str. 91001]

ref|YP_652279.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
Antiqua]
31 more sequence titles

ref|YP_647139.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pesti
Nepal516]

ref|YP_001162910.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
Pestoides F]

ref|ZP_01887420.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
CA88-41Z5]

ref|YP_001607938.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
Angola]

ref|ZP_02224083.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Orientalis str. F1991016]

ref|ZP_02227818.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Orientalis str. IP275]

ref|ZP_02228990.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Antiqua str. E1979001]

ref|ZP_02238376.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Antiqua str. B42003004]

ref|ZP_02304312.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Antiqua str. UG05-0454]

ref|ZP_02313105.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Orientalis str. MG05-1020]

ref|ZP_02315362.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
biovar Mediaevalis str. K1973002]

ref|ZP_02332413.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pest
FV-1]

ref|YP_001719943.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
YPIII]

ref|YP_002347860.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
CO92]

sp|Q8ZCP4.1|PDXJ_YERPE RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN

gb|AAM84874.1|AE013732_6 **G** pyridoxine biosynthesis [Yersinia pestis KIM]

gb|AAS62723.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis
biovar Microtus str. 91001]

gb|ABG17539.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Nepal516]
 gb|ABG14334.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Antiqua]
 emb|CAL21538.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pesti C092]
 gb|ABP39937.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Pestoides F]
 gb|EDM41872.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis CA88-4125]
 gb|ABX88699.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis Angola]
 gb|EDR31495.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Orientalis str. IP275]
 gb|EDR37091.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Orientalis str. F1991016]
 gb|EDR44775.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Antiqua str. E1979001]
 gb|EDR50752.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Antiqua str. B42003004]
 gb|EDR56862.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Orientalis str. MG05-1020]
 gb|EDR62700.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Antiqua str. UG05-0454]
 gb|EDR67525.1| pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis biovar Mediaevalis str. K1973002]
 gb|ACA67490.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudo YPIII]
 Length=243

GENE ID: 1146247 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pestis KIM] (10 or fewer PubMed links)

Score = 391 bits (1005), Expect = 2e-107, Method: Compositional matrix adjust.
 Identities = 197/242 (81%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Sbjct	1	MA+LLLGVNIDHIATLRNARGT YDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
Sbjct	61	LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIIPMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	YAAAGKGLKVNAGHGLTYHNVQPIAALPEMHELNIGHAIIGQAVMTGLAAAVTDMKVLRE	240
Query	241	AR	242
Sbjct	241	AR	242

>pdb|3F4N|A **S** Chain A, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|B **S** Chain B, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|C **S** Chain C, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|D **S** Chain D, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|E **S** Chain E, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|F **S** Chain F, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|G **S** Chain G, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis

pdb|3F4N|H S Chain H, Crystal Structure Of Pyridoxal Phosphate Biosynthetic Protein Pdxj From Yersinia Pestis
Length=246

Score = 391 bits (1005), Expect = 3e-107, Method: Compositional matrix adjust.
Identities = 197/242 (81%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI
Sbjct 4  MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 63

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A
Sbjct 64  LRQTIQTRMNLEMAVTDEMVDIACDIKPHFCCLVPEKRQEVTTTEGGLDVAGQVDKMTLAV 123

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          RLAD GI VSLFIDAD QI AA GAP+IEIHTG YADA T E+ EL RIAKAAT
Sbjct 124  GRLADVGVILVSLFIDADFRQIDAAVAAGAPYIEIHTGAYADASTVLERQAEMLRIKAAT 183

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AA GLKVNAGHGLTYHNV+ IAA+PEMHENLIGHAIIG+AVMTGL AV +MK LM E
Sbjct 184  YAAGKGLKVNAGHGLTYHNVQPIAALPEMHENLIGHAIIGQAVMTGLAAAVTDMKVLRE 243

Query 241  AR 242
          AR
Sbjct 244  AR 245

```

>ref|ZP_00833834.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 29909]
Length=243

Score = 390 bits (1003), Expect = 4e-107, Method: Compositional matrix adjust.
Identities = 195/242 (80%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI
Sbjct 1  MADLLLGVNIDHIATLRNARGTIYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A
Sbjct 61  LRQTIQTRMNLEMAVTDEMVDIACELQPHFCCLVPEKRQEVTTTEGGLDVAGQLDKMTIAV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          RL++AGI VSLFID D QI AA VGAP+IEIHTG YADA TD + EL RI KAAT
Sbjct 121  SRLSEAGILVSLFIDPDMRQIDAAVAVGAPYIEIHTGAYADATTDLVRQAEVLVITKAAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AA GLKVNAGHGLTYHNV+ IAA+PEMHENLIGHAIIG+AVMTGL AV +MK LM E
Sbjct 181  YAAGKGLKVNAGHGLTYHNVQPIAALPEMHENLIGHAIIGQAVMTGLAAAVTDMKVLRE 240

Query 241  AR 242
          AR
Sbjct 241  AR 242

```

>ref|ZP_00827187.1| COG0854: Pyridoxal phosphate biosynthesis protein [Yersinia ATCC 43969]
Length=243

Score = 390 bits (1003), Expect = 4e-107, Method: Compositional matrix adjust.
Identities = 195/242 (80%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          MA+LLLGVNIDHIATLRNARGT YPDP+QAAAFIAEQAGADGITVHLREDRRHITDRDVRI
Sbjct 1  MADLLLGVNIDHIATLRNARGTIYPDPIQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKRQEVTTTEGGLDVAGQ DKM A
Sbjct 61  LRQTIQTRMNLEMAVTDEMVGIACELQPHFCCLVPEKRQEVTTTEGGLDVAGQIDKMTIAV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          RLA+AGI VSLFIDAD QI AA VGAP+IEIHTG YADA TD + EL RI KAAT
Sbjct 121  SRLAEAGILVSLFIDADMRQIDAAVTVGAPYIEIHTGAYADAITDLARQAEVLVITKAAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AAS GLKVNAGHGLTYHNV+ IAA+PE+ ELNIGHAIIG+AVMTGL AV +MK LM E
Sbjct 181  YAASKGLKVNAGHGLTYHNVQPIAALPEIQELNIGHAIIGQAVMTGLAAAVGDMKVLRE 240

```

Query 241 AR 242
 AR
 Sbjct 241 AR 242

>ref|YP_071394.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseu
 IP 32953]
 ref|YP_001873412.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia p
 PB1/+]
 sp|Q3V7P0.1|PDXJ YERPS RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 emb|CAH22125.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseud
 IP 32953]
 gb|ACC89955.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Yersinia pseudo
 PB1/+]
 Length=243

GENE ID: 2956225 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
 [Yersinia pseudotuberculosis IP 32953] (10 or fewer PubMed links)

Score = 390 bits (1003), Expect = 4e-107, Method: Compositional matrix adjust.
 Identities = 196/242 (80%), Positives = 208/242 (85%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIIVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDRDKMRDAC	120
Sbjct	61	LRQT+ TRMNLEMAVT+EM+ IA + KPHFCCLVPEKRQEVTTTEGGLDVAGQ DKM	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	RLAD GI VSLFIDAD QI AA GAP+IEIHTG YADA T E+ EL RIAKAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	+AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIG+AVMTGL AV +MK LM E	240
Query	241	AR 242	
Sbjct	241	AR 242	

>ref|YP_051364.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Pectobacteriu
 atrosepticum SCRI1043]
 sp|Q3V7N3.1|PDXJ ERWCT RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 emb|CAG76173.1| **G** pyridoxal phosphate biosynthetic protein [Pectobacterium atro
 SCRI1043]
 Length=243

GENE ID: 2882129 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ
 [Pectobacterium atrosepticum SCRI1043] (10 or fewer PubMed links)

Score = 390 bits (1001), Expect = 7e-107, Method: Compositional matrix adjust.
 Identities = 194/242 (80%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query	1	MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
Sbjct	1	MAELLLGVNIDHIATLRNARGT YPDPVQAAF+AEQAGADGITVHLREDRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIIVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDRDKMRDAC	120
Sbjct	61	LR+TL TRMNLEMAVTEEML IA E KPHFCCLVPEKRQEVTTTEGGLDVAGQ++K+ +A	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	RL+ A I VSLFIDAD+ QI AA GA +IEIHTG YADA D + E RI AAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	+AA+ GLKVNAGHGLTYHNV IAA+PEMHELNIGHAIIGRAV++GLKDAVAEMK LM E	240
Query	241	AR 242	
Sbjct	241	AR 242	

>ref|YP_001479890.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Serratia p 568]

gb|ABV42762.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Serratia protea 568]
Length=243

GENE ID: 5606405 Spro_3666 | pyridoxal phosphate biosynthetic protein PdxJ [Serratia proteamaculañs 568]

Score = 382 bits (981), Expect = 1e-104, Method: Compositional matrix adjust.
Identities = 192/242 (79%), Positives = 209/242 (86%), Gaps = 0/242 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Sbjct	1	MA+LLLGVNIDHIATLRNARGT YPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQQRDKMRDAC	120
Sbjct	61	LRQT+ TRMNLEMAVT+EML IA+E KPHFCCLVPEKR+EVTTTEGGLDVAGQ+DKM A	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	++LA AGI VSLFID D QI AA VGAP+IEIHTG YA+A+ + EL RIA AAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	+AA GLKVNAGHGLTYHNV+ IAA+PEMHELNIGHAIIIG+AVM GL AV +MK LM E	240
Query	241	AR	242
Sbjct	241	AR	242

>ref|YP_455464.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Sodalis gloss str. 'morsitans']

dbj|BAE75059.1| **G** pyridoxal phosphate biosynthetic protein [Sodalis glossinidius str. 'morsitans']
Length=243

GENE ID: 3866528 SG1784 | pyridoxal phosphate biosynthetic protein PdxJ [Sodalis glossinidius str. 'morsitans'] (10 or fewer PubMed links)

Score = 381 bits (978), Expect = 3e-104, Method: Compositional matrix adjust.
Identities = 187/242 (77%), Positives = 208/242 (85%), Gaps = 0/242 (0%)

Query	1	MAELLLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
Sbjct	1	M+ELLLLGVNIDHIATLRNARG A+PDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDV++	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQQRDKMRDAC	120
Sbjct	61	LR+T+ TRMNLEMAVTEEM++IA+ PHFCCLVPEKRQEVTTTEGGLDVAGQ DK+R A	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
Sbjct	121	L+ AGIQVSLFIDADE QI AAA+VGAP+IEIHTG YADA + +A E ARI + A	180
Query	181	FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIIGRAVMTGLKDAVAEMKRLMLE	240
Sbjct	181	FA LGLKVNAGHGL YHNVK +AA+ +M ELNIGHAII RAV+ GL DAV +MKRLM E	240
Query	241	AR	242
Sbjct	241	AR	242

>ref|NP_930557.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Photorhabdus subsp. laumondii TT01]

sp|Q7N1X8.1|PDXJ PHOLL RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
emb|CAE15711.1| **G** Pyridoxal phosphate biosynthetic protein PdxJ (PNP synthase) [Photorhabdus luminescens subsp. laumondii TT01]
Length=243

GENE ID: 2803349 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Photorhabdus luminescens subsp. laumondii TT01] (10 or fewer PubMed links)

Score = 376 bits (966), Expect = 7e-103, Method: Compositional matrix adjust.
Identities = 184/242 (76%), Positives = 208/242 (85%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          MAE+LLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGIT+HLREDRRHITDRDV +
Sbjct 1  MAEVLGVNIDHIATVRNARGTHYPDPVQAAFVAEQAGADGITIHLREDRRHITDRDVEL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          L++T+ TRMNLEMAVT+EM+ IA KP FCCLVPEKRQEVTTTEGGLDV GQ+DK+ A
Sbjct 61  LKKTIQTRMNLEMAVTDEMVDIACRIKPEFCCLVPEKRQEVTTTEGGLDVIGQKDKVAAAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          KRL+DAGI VSLFIDA+ QI AA EVGAFFIEIHTG YADAK + EQ +E RI AAT
Sbjct 121 KRLSDAGILVSLFIDAHEHRQIDAANEVGAFFIEIHTGAYADAKNEVEQEKEFHRIKAAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AAS GL VNAGHGLTYHNV+ IAA+PE++ELNIGHAIIGRAV +GL AVA+MK M +
Sbjct 181 YAASKGLTVNAGHGLTYHNVQRIAAALPEIYELNIGHAIIGRAVFSGLTAAVADMKTQMRK 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|YP_855346.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas hydrophila ATCC 7966]

gb|ABK38566.1| G pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas hydrophila ATCC 7966]
Length=245

GENE ID: 4487304 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Aeromonas hydrophila subsp. hydrophila ATCC 7966] (10 or fewer PubMed links)

Score = 376 bits (965), Expect = 9e-103, Method: Compositional matrix adjust.
Identities = 187/242 (77%), Positives = 203/242 (83%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+E+ LGVNIDHIATLRNARGT YPDPVQAAF+AEQAGADGITVHLREDRRHITDRDV I
Sbjct 1  MSEIYLGVNIDHIATLRNARGTQYPDPVQAAFVAEQAGADGITVHLREDRRHITDRDVEI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          LRQT+ TRMNLEMAVTEEM+ IA +PHF CLVPEKR EVTTTEGGLDVAGQ DK+ DA
Sbjct 61  LRQTIQTRMNLEMAVTEEMIGIACRIQPHFVCLVPEKRTEVTTEGGLDVAGQLDKVTDVAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RL+ G QVSLFIDAD QI AAAE GAPFIEIHTG YADA TDAE+ E RIA A+
Sbjct 121 ARLSAVGAQVSLFIDADPLQIDAAAESGAPFIEIHTGRYADATTTDAERNAEFKRIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AA GLKVNAGHGL YHNVKAIAAIPE++ELNIGHAIIGRA GL AV++M+ LM E
Sbjct 181 YAAGKGLKVNAGHGLHYHNVKAIAAIPELYELNIGHAIIGRAAFDGLAKAVSDMRLLMQE 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_03318787.1| hypothetical protein PROVALCAL_01725 [Providencia alcalifaciens DSM 30120]

gb|EEB46268.1| hypothetical protein PROVALCAL_01725 [Providencia alcalifaciens DSM 30120]
Length=243

Score = 373 bits (958), Expect = 7e-102, Method: Compositional matrix adjust.
Identities = 180/242 (74%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          MAELLLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGIT+HLREDRRHITDRDV +
Sbjct 1  MAELLLGVNIDHIATVRNARGTQYPDPVQAAFVAEQAGADGITIHLREDRRHITDRDVEL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          L +T+ TRMNLEMAVTEEM+ IA KP +CCLVPEKR+EVTTTEGGLDVAGQ+ K+ A
Sbjct 61  LNKTIQTRMNLEMAVTEEMIDIACRIKPTYCCLVPEKREEVTTTEGGLDVAGQKQKVAFAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180

```

```

Sbjct 121 KRL DAGI VSLFIDAD +QI AA E GAPFIEIHTG YADAKT+ EQ E RI +
KRLTDAGILVSLFIDADHKQIDAAQECGAPFIEIHTGAYADAKTEQEQELEFRIRRDGVS 180
Query 181 FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AA G+KVNAGHGLTYHNV+ IAA+PE++ELNIGHAIIGRA+ +GL AV++MK L++E
Sbjct 181 YAAGGIKVNAGHGLTYHNVQRIALLPEIYELNIGHAIIGRALFSGLSQAVSDMKNLLIE 240
Query 241 AR 242
AR
Sbjct 241 AR 242

```



>ref|ZP_02961267.1| hypothetical protein PROSTU_03281 [Providencia stuartii ATCC 25827]
 gb|EDU60077.1| hypothetical protein PROSTU_03281 [Providencia stuartii ATCC 25827]
 Length=243

Score = 373 bits (957), Expect = 7e-102, Method: Compositional matrix adjust.
 Identities = 182/242 (75%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
MAELLLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGITVHLREDRRRHITDRD+ +
Sbjct 1 MAELLLGVNIDHIATVRNARGTQYPDPVQAAFFVAEQAGADGITVHLREDRRRHITDRDIEL 60
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
L++T+ TRMNLEMAVTEEM+ IA KP FCCLVPEKR+EVTTTEGGLDVAGQ K+ DA
Sbjct 61 LKETIQTRMNLEMAVTEEMINIAICRVKPAFCCLVPEKREEVTTTEGGLDVAGQLPKITDAV 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
KRL+AGIQVSLFIDAD QI AA GAPFIEIHTG YADAKT+ EQ E RI
Sbjct 121 KRLTEAGIQVSLFIDADHTQIDAAQAAGAPFIEIHTGAYADAKTEQEQEIEYRRIRRDGVA 180
Query 181 FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AA GLKVNAGHGLTYHNV+ IA +PE++ELNIGHAIIGRA+ +GL +AVA+MK+L+ E
Sbjct 181 YAAGKGLKVNAGHGLTYHNVQRIALLPEIYELNIGHAIIGRALFSGLANAVADMKKLLRE 240
Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|YP_002151612.1|  pyridoxal phosphate biosynthetic protein [Proteus mirabil
 emb|CAR43908.1|  pyridoxal phosphate biosynthetic protein [Proteus mirabilis H
 Length=243



GENE ID: 6803577 **pdxJ** | pyridoxal phosphate biosynthetic protein
 [Proteus mirabilis HI4320] (10 or fewer PubMed links)

Score = 372 bits (956), Expect = 1e-101, Method: Compositional matrix adjust.
 Identities = 181/242 (74%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
M+++LLGVNIDHIATLRNARGT YPDPVQAAFIQAGADGITHLREDRRRHITDRD+ +
Sbjct 1 MSDILLGVNIDHIATLRNARGTTYPDPVQAAFIQAGADGITHLREDRRRHITDRDML 60
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
+ QT+ TR+NLEMAVTEEM+ IA +T+P FCCLVPEKRQEVTTTEGGLDV G +K+ DA
Sbjct 61 ISQTVQTRLNLEMAVTEEMIEIACQTPDFCCLVPEKRQEVTTTEGGLDVVGNEEKVADAI 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
KRL+ AGI+VSLFID D EQI AA VGAPFIEIHTG YADA+ + Q +E RI A T
Sbjct 121 KRLSLAGIKVSLFIDPDHEQINAAADRVGAPFIEIHTGAYADAEDAQAQKEFVRIRDAVT 180
Query 181 FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AAS GLKVNAGHGL YHNV+ IAA+PE++ELNIGHAIIGRAV +GL AV EMKRLM E
Sbjct 181 YAASKGLKVNAGHGLHYHNVQRIALLPELYELNIGHAIIGRAVFSGLAPAVEEMKRLMRE 240
Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|YP_001143199.1|  pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas
 subsp. salmonicida A449]
 gb|AB091451.1|  pyridoxal phosphate biosynthetic protein PdxJ [Aeromonas salmo
 subsp. salmonicida A449]

Length=245

GENE ID: 4996852 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Aeromonas salmonicida subsp. salmonicida A449]

Score = 372 bits (954), Expect = 2e-101, Method: Compositional matrix adjust.
Identities = 184/242 (76%), Positives = 201/242 (83%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+E+ LGVNIDHIATLRNARGT YPDPVQAAF+AEQAGADGITVHLREDRRRHITDRDV I
Sbjct 1  MSEIYLGVNIDHIATLRNARGTQYPDPVQAAFVAEQAGADGITVHLREDRRRHITDRDVEI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LRQT+ TRMNLEMAVTEEM+ IA KPHF CLVPEKR EVTTEGGLDVAGQ DK+ DA
Sbjct 61  LRQTIQTRMNLEMAVTEEMIGIACRIKPHFVCLVPEKRTEVTTTEGGLDVAGQLDKITDAV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RL+ G QVSLFIDAD QI AAA+ GAPFIEIHTG YADA TD ++ E RIA A+
Sbjct 121  TRLSAVGAQVSLFIDADPLQIDAAADSGAPFIEIHTGRYADATTTDRNAEFKRIAAGAS 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AA GLKVNAGHGL YHNVKAIAAIP++ELNIGHAIIGRA GL AV++M+ LM E
Sbjct 181  YAAGKGLKVNAGHGLHYHNVKAIAAIPELYELNIGHAIIGRAAFDGLTKAVSDMRLLMQE 240

Query 241  AR 242
          R
Sbjct 241  VR 242

```

>ref|ZP_03315319.1| hypothetical protein PROVRUST_02121 [Providencia rustigianii DSM 454T]

gb|EEB38919.1| hypothetical protein PROVRUST_02121 [Providencia rustigianii DSM 4541]

Length=243

Score = 367 bits (942), Expect = 4e-100, Method: Compositional matrix adjust.
Identities = 178/242 (73%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          MAELLLGVNIDHIAT+RNARGT YPDPVQAAF+AEQAGADGIT+HLREDRRRHITDRDV +
Sbjct 1  MAELLLGVNIDHIATVRNARGTQYPDPVQAAFVAEQAGADGITIHLREDRRRHITDRDVEL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          L QT+ TRMNLEMAVT+EM+ IA KP +CCLVPEKR+EVTTTEGGLDVAGQ+ K+ A
Sbjct 61  LNQTIQTRMNLEMAVTDEMIDIACRIKPTYCCLVPEKREEVTTTEGGLDVAGQKQKVAAAV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          KRL ++GI VSLFIDAD EQI AA E GAPFIEIHTG YADAKT+ Q E RI
Sbjct 121  KRLTESGILVSLFIDADHEQIDAAQECGAPFIEIHTGAYADAKTEQAQEIEFRRIRDGVK 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AA G+KVNAGHGLTYHNV+ IAA+PE++ELNIGHAIIGRA+ +GL AV++MK+L+ E
Sbjct 181  YAAGKGIKVNAGHGLTYHNVQRIALPEIYELNIGHAIIGRALFSLAQAVSDMKQLLTE 240

Query 241  AR 242
          AR
Sbjct 241  AR 242

```

>ref|ZP_01262022.1| pyridoxal phosphate biosynthetic protein [Vibrio alginolytic 12G01]

gb|EAS74655.1| pyridoxal phosphate biosynthetic protein [Vibrio alginolyticus 12G01]

Length=244

Score = 361 bits (926), Expect = 3e-98, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRRHITDRDVRI
Sbjct 1  MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LR+T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGLDV GQ +K++ A
Sbjct 61  LRETIQTRMNLEMAVTDEMIEIALQTKPEFVCLVPEKREELTTEGGLDVVGQLEKIKAAAT 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          K+L DAGI+VSLFIDAD +QI+AA + GAPFIE+HTG YADA T+ EQ EL +IA A+
Sbjct 121  KKLTDAGIKVSLFIDADRQQIEAAKCGAPFIELHTGHYADATTEDEQQQELKKIAAGAS 180

```

```

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL AVA+MK LM+E
Sbjct 181 YAHDLGIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLNKAVADMKALMIE 240

Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|ZP_03385196.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella enterica serovar Typhi str. M223]
Length=192

Score = 360 bits (925), Expect = 4e-98, Method: Compositional matrix adjust.
Identities = 179/192 (93%), Positives = 183/192 (95%), Gaps = 0/192 (0%)

```


Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTDYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60



Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
LRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC
Sbjct 61 LRQTLHTRMNLEMAVTEEMLAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
RLA AGIQVSLFIDADE QI AAAEEVGAPFIEIHTGICYA+A+TDAEQA+ELARIA AAT
Sbjct 121 ARLAAAGIQVSLFIDADERQINAAAEEVGAPFIEIHTGICYANAETDAEQAKELARIAASAAT 180

Query 181 FAASLGLKVNAG 192
AA LGLKVNAG
Sbjct 181 LAARLGLKVNAG 192

```

>ref|YP_205467.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri ES114]

sp|Q5E317.1|PDXJ VIBF1  RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
gb|AAW86579.1|  pyridoxine 5'-phosphate synthase [Vibrio fischeri ES114]
Length=243

GENE ID: 3279332 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Vibrio fischeri ES114] (10 or fewer PubMed links)

Score = 360 bits (924), Expect = 5e-98, Method: Compositional matrix adjust.
Identities = 173/242 (71%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
M+ +LLGVNIDH+ATLRNARGT YPDPV AA IAE+AGA GIT+HLREDRRHI DRDVRI
Sbjct 1 MSSILLGVNIDHVATLRNARGTKYPDPVHAAEIAERAGAAGITIHLEDRRRHIKDRDVRI 60



Query 61 LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC 120
LR+TL TRMNLEMAVT+EM+ IA+ETKP F CLVPEKR+E+TTEGGL+V+GQ +K++ A
Sbjct 61 LRETQLQTRMNLEMAVTDEMVGIALETKPEFVCLVPEKREELTTEGGLNVSGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
++L +AGI+VSLFIDAD+EQI AA E GAPFIE+HTG YADA+T+ Q EL +IA A+
Sbjct 121 QKLTEAGIKVSLFIDADKEQIDAAVECGAPFIELHTGAYADAETEEAQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AAS GL VNAGHGLTYHNV+AIAA+PE++ELNIGH+I+GRA+ GL+ AVA+M R+ML
Sbjct 181 YAASKGLIVNAGHGLTYHNVAAIPEIYELNIGHSIMGRAMFDGLEKAVADMHRIMLG 240

Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|YP_002073491.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio sp.
gb|EDN55839.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio sp. Ex25]
Length=243

GENE ID: 6654483 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Vibrio sp. Ex25]

Score = 358 bits (920), Expect = 1e-97, Method: Compositional matrix adjust.
Identities = 173/242 (71%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ + LGVNIDHIATLRNARGT YDPDV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHILDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
      LR+T+ TRMNLEMAVT+EM+ IA++T+P F CLVPEKR+E+TTEGGLDV GQ +K++ A
Sbjct 61 LRETIQTRMNLEMAVTDEMVEIALQTQPEFVCLVPEKREELTTEGGLDVVGQLEKIKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      K+L DAGI+VSLFIDAD +QI+AA + GAPFIE+HTG YADA T+ EQ EL +IA A+
Sbjct 121 KKLTDAGIKVSLFIDADRQQIEAAKKGAPFIELHTGHYADATTEDEQQAELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL AVA+MK LM+E
Sbjct 181 YAHDLGIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLNKAVADMKALMIE 240

Query 241 AR 242
      AR
Sbjct 241 AR 242

```

>ref|YP_002156883.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fis MJ11]

gb|ACH66587.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri MJ11]

Length=243

GENE ID: 6806102 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio fischeri MJ11]

Score = 358 bits (919), Expect = 2e-97, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 210/242 (86%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ +LLGVNIDH+ATLRNARGT YDPDV AA IAE+AGA GIT+HLREDRRHI DRDVRI
Sbjct 1 MSSILLGVNIDHVATLRNARGTKYPDPVHAAEIAERAGAAGITIHLEDRRRHIKDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
      LR+TL TRMNLEMAVT+EM+ IA+ETKP F CLVPEKR+E+TTEGGL+V+GQ +K++ A
Sbjct 61 LRETLQTRMNLEMAVTDEMVGIALETKPEFVCLVPEKREELTTEGGLNVSGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      ++L +AGI+VSLFIDAD++QI AA E GAPFIE+HTG YADA+T+ Q EL +IA A+
Sbjct 121 QKLTEAGIKVSLFIDADKKQIDAAVECGAPFIELHTGAYADAETEEAQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +AAS GL VNAGHGLTYHNV+AIAA+PE++ELNIGH+I+GRA+ GL+ AV++M R+ML
Sbjct 181 YAASKGLIVNAGHGLTYHNVVEAIAALPEIYELNIGHSIMGRAMFDGLEKAVSDMHRIMLG 240

Query 241 AR 242
      AR
Sbjct 241 AR 242

```

>ref|ZP_03400922.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en subsp. enterica serovar Typhi str. AG3].
Length=191

Score = 357 bits (916), Expect = 5e-97, Method: Compositional matrix adjust.
Identities = 176/191 (92%), Positives = 183/191 (95%), Gaps = 0/191 (0%)

```

Query 53 ITDRDVRILRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ 112
      +TDRDVRILRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEKRQEVTTTEGGLDVAGQ
Sbjct 1 MTDRDVRILRQTLHTRMNLEMAVTEEMLAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQ 60

Query 113 RDKMRDACKRLADAGIQVSLFIDADEEQIKAAAEEVGAPFIEIHTGCIYADAKTDAEQAQEL 172
      RDKMRDAC RLA AGIQVSLFIDADE QI AAAEEVGAPFIEIHTGCIY+A+TDAEQ+A+EL
Sbjct 61 RDKMRDACARLAAAGIQVSLFIDADERQINAAAEEVGAPFIEIHTGCIYANAETDAEQAKEL 120

Query 173 ARIAKAATFAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVA 232
      ARIA AAT AA LGLKVNAGHGLTYHNVKAAIAA+PEMHELNIGHAIIGRAVMTGLK+AVA
Sbjct 121 ARIASAATLAARLGLKVNAGHGLTYHNVKAAIAALPEMHELNIGHAIIGRAVMTGLKEAVA 180

Query 233 EMKRLMLEARG 243
      EMKRLMLEARG
Sbjct 181 EMKRLMLEARG 191

```

>ref|NP_760465.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio vulnif CMCP6]
 ref|NP_935621.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio vulnif YJ016]
 sp|Q8DC73.1|PDXJ_VIBVU RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 sp|Q7MHP1.1|PDXJ_VIBVY **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
 gb|AA009992.1|AE016802_35 **G** Pyridoxal phosphate biosynthesis protein [Vibrio vu
 dbj|BAC95592.1| **G** pyridoxal phosphate biosynthesis protein [Vibrio vulnificus Y
 Length=243

GENE ID: 1178481 VV1 1568 | pyridoxal phosphate biosynthetic protein PdxJ
 [Vibrio vulnificus CMCP6] (10 or fewer PubMed links)

Score = 356 bits (914), Expect = 9e-97, Method: Compositional matrix adjust.
 Identities = 172/242 (71%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M+ + LGVNIDH+ATLRNARGT YDPDV AA +AE+AGADGIT+HLREDRRHITDRDVRI	
Sbjct	1	MSSIY LGVNIDHVATLRNARGTKYPDPVHAAEVAERAGADGITIHLREDRRHITDRDVRI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDVAG DK++ A	
Sbjct	61	LRET LQTRMNLEMAVTDEMIEIALKTQPEYVCLVPEKREELTTEGGLDVAGHLDKIKAAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		++L AGI+VSLFIDAD EQI AA GAPFIE+HTG YADA T+A+Q EL +IA A+	
Sbjct	121	EKLTAAGIKVSLFIDADREQIDAACACGAPFIELHTGHYADAATEADQLDELKKIAAGAS	180
Query	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+AA LG+ VNAGHGLTYHNV IAA+PE++ELNIGHAIIGRAV GL AVA+MK +M+	
Sbjct	181	YAADLGITVNAGHGLTYHNVAPIAALPEIYELNIGHAIIGRAVFDGLHKAVADMKAIMVA	240
Query	241	AR	242
		AR	
Sbjct	241	AR	242

>ref|YP_131204.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Photobacteriu profundum SS9]
 sp|Q3V7I6.1|PDXJ PHOPR RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 emb|CAG21402.1| **G** putative pyridoxal phosphate biosynthetic protein PdxJ [Photob profundum SS9]
 Length=243

GENE ID: 3123572 PBPRA3086 | pyridoxal phosphate biosynthetic protein PdxJ
 [Photobacterium profundum SS9] (10 or fewer PubMed links)

Score = 355 bits (912), Expect = 1e-96, Method: Compositional matrix adjust.
 Identities = 172/242 (71%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M +LLGVNIDHIATLRNARGT YDPDV AA +AE+AGADGITVHLREDRRHI DRDVRI	
Sbjct	1	MNNILLGVNIDHIATLRNARGTRYPDPVHAAEVAERAGADGITVHLREDRRHINDRDVRI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		L++T+ TRMNLEMAVT+EM++IA++TKP F CLVPEKR+E+TTEGGLDVAGQ +K++ A	
Sbjct	61	LKETIQTRMNLEMAVTDEMVSIALDTKPEFVCLVPEKREELTTEGGLDVAGQLEKIKAAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		++L DAGI+VSLFIDAD QI A GAPF+E+HTG YADA+T+ Q EL +IA AAT	
Sbjct	121	QKLT DAGIKVSLFIDADRAQIDATLACGAPFVELHTGHYADAETEEAQQAELEKIASAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A LG+KVNAGHGLTYHNVK IAA+PE++ELNIGH+II RA GL AVA+MK ML+	
Sbjct	181	YAHGLGIKVNAGHGLTYHNVKPIAALPELYELNIGHSIISRAAFDGLNKAVADMKVEMLD	240
Query	241	AR	242
		AR	
Sbjct	241	AR	242

>ref|ZP_01816562.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrionales b SWAT-3]
 gb|EDK26047.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrionales bacte SWAT-3]

Length=245

Score = 354 bits (909), Expect = 3e-96, Method: Compositional matrix adjust.
 Identities = 171/243 (70%), Positives = 204/243 (83%), Gaps = 0/243 (0%)

```


Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+ +LLGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1  MSSILLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRRHIVDRDVRI 60


Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC 120
          L +T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGGLDV GQ DK++ A
Sbjct 61  LAETIQTRMNLEMAVTDEMVDQIALDTKPEFVCLVPEKREELTTEGGGLDVVGQLDKIKAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          ++L++AGI+VSLFIDAD EQI AA GAPFIE+HTG YADAKT+ +Q EL +IA A+
Sbjct 121 QKLSEAGIKVSLFIDADREQIDAACACGAPFIELHTGHYADAKTEEDQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+I+GRAV GL AVA+MK +M
Sbjct 181 YADDLGITVNAGHGLTYHNVAPIAALPEIYELNIGHSIMGRAVFDGLNKAVADMKAVMET 240

Query 241 ARG 243
          AR
Sbjct 241 ARN 243
  
```

>ref|YP_001906938.1|  Pyridoxal phosphate biosynthetic protein (PNP synthase) [tasmaniensis Et1/99]

emb|CA096041.1|  Pyridoxal phosphate biosynthetic protein (PNP synthase) [Erwinia tasmaniensis Et1/99]
 Length=243

GENE ID: 6299767 pdxJ | Pyridoxal phosphate biosynthetic protein (PNP synthase) [Erwinia tasmaniensis Et1/99]

Score = 354 bits (908), Expect = 4e-96, Method: Compositional matrix adjust.
 Identities = 186/243 (76%), Positives = 205/243 (84%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          MAELLLGVNIDH+AT+RNARGT YPDPVQAAAF++EQAGADGITVHLREDRRHI DRDVRI
Sbjct 1  MAELLLGVNIDHVATVRNARGTNYDPVQAAAFVSEQAGADGITVHLREDRRHINDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC 120
          LRQT+ TRMNLEMAVT+EM+ IA E +PHFCCLVPEKR+EVTEGGGLDVAGQ DK+ A
Sbjct 61  LRQTIQTRMNLEMAVTDEMVDIACEIQPHFCCLVPEKREEVTTEGGGLDVAGQLDKVTA AV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          KRL DAG+ VSLFIDAD QI AA GAP+IEIHTG YA+A + ELARIA AAT
Sbjct 121 KRLNDAGVLVSLFIDADRGQIDAABAAGAPYIEIHTGAYAEAPEGLARDELTARIAAAAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +AA GLKVNAGHGLTYHNV IAA+PEM ELNIGHAIIGRAV +GL AV EMK+L+
Sbjct 181 YAAGKGLKVNAGHGLTYHNVLPAAALPEMVELNIGHAIIGRAVFSGLAAAVQEMKQLLRA 240

Query 241 ARG 243
          ARG
Sbjct 241 ARG 243
  
```

>ref|ZP_01161526.1| pyridoxal phosphate biosynthetic protein [Photobacterium sp. SKA34]

gb|EAR54737.1| pyridoxal phosphate biosynthetic protein [Photobacterium sp. SKA34]
 Length=243

Score = 353 bits (906), Expect = 7e-96, Method: Compositional matrix adjust.
 Identities = 168/243 (69%), Positives = 208/243 (85%), Gaps = 0/243 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M +LLGVNIDHIATLRNARGT+YPDPV AA +AE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1  MNNILLGVNIDHIATLRNARGTSYPDPVHAAEVAERAGADGITIHLREDRRHINDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC 120
          LR+T+ TRMNLEMAVT+EM+AIA++ KP + CLVPEKR+E+TTEGGGLDV+GQ +K++ A
Sbjct 61  LRETIQTRMNLEMAVTDEMVAIALDVKPEYVCLVPEKREELTTEGGGLDVSGQLEKVKAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
          ++L AGI+VSLFIDAD QI AA GAPFIE+HTG YA+AKT+ Q EL ++A A+
  
```

```

Sbjct 121 EKLTAAGIKVSLFIDADRAQIDAAHACGAPFIELHTGQYAEAKTEEAQLDELKKVAAGAS 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIIP+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E 240
          +A +LG+KVNAGHGLTYHNVK IAA+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E
Sbjct 181 YAHNLGIKVNAGHGLTYHNVKLI AALPELYELNIGHSIMGRAMFDGLEKSVADMRLLMQE 240
Query 241 ARG 243
          ARG
Sbjct 241 ARG 243

```

>ref|YP_002127690.1| **G** pyridoxal phosphate biosynthetic protein [Alteromonas mac
'Deep ecotype']

gb|ACG67696.1| **G** pyridoxal phosphate biosynthetic protein [Alteromonas macleodi
'Deep ecotype']
Length=250

GENE ID: 6778911 MADE 03404 | pyridoxal phosphate biosynthetic protein
[Alteromonas macleodii-'Deep ecotype'] (10 or fewer PubMed links)

Score = 353 bits (905), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 202/242 (83%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLRNARGT YDPV AA IAE+AGADGITVHLREDRRHI DRDVRI
Sbjct 6 MSTILLGVNIDHIATLRNARGTHYPDPVHAADIAERAGADGITVHLREDRRHIKDRDVRI 65
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDRDKMRDAC 120
          L QT++TR+NLEMAVT+EMLAIA E KP FCCLVPEKR+E+TTEGGLDVAG D ++ AC
Sbjct 66 LAQTINTRLNLEMAVTDEMLAIAEEVKPVFCCLVPEKREELTTEGGLDVAGNVNDNIKAAC 125
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RLA+A I VSLFIDAD+ QI AAA AP+IEIHTG YA+A ++ Q +ELAR+ +
Sbjct 126 DRLANANILVSLFIDADKAQIDAAAACNAPYIEIHTGQYAEATSEEAQQEELARLVEGIE 185
Query 181 FAASLGLKVNAGHGLTYHNVKAIIP+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E 240
          +A SLGLKVNAGHGL YHNVK IAAIP++ ELNIGH+I+RA GL AVA+M++LMLE
Sbjct 186 YADSLGLKVNAGHGLHYHNVKPIAAIPQLIELNIGH+I+RAA+FDGLHKAVADMRLKMLE 245
Query 241 AR 242
          AR
Sbjct 246 AR 247

```

>ref|ZP_01870295.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio shilon
AK1]

gb|EDL51107.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio shilonii
AK1]
Length=244

Score = 352 bits (904), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 170/242 (70%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLG+NIDHIATLRNARGT YDPV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MSSILLGINIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHILDRDVRI 60
Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDRDKMRDAC 120
          LR+TL TRMNLEMAVT+EM+ IA++T+P F CLVPEKR+E+TTEGGLDV GQ +K++ A
Sbjct 61 LRETQLQTRMNLEMAVTDEMIDIALKTQPEFVCLVPEKREELTTEGGLDVKGQLEKIKAAAT 120
Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L+ AGI+VSLFIDAD EQI AA GAPFIE+HTG YADA+T+ +Q EL +IA A+
Sbjct 121 EKLSAAGIKVSLFIDADREQIDAAKAAGAPFIELHTGHYADAETEEDQQDELKKIAAGAS 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIIP+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E 240
          +AA +G+ VNAGHGLTYHNV IAA+PE++ELNIGH+I+GRAV GL AVA+MK +M
Sbjct 181 YAADIGITVNAGHGLTYHNVAPIAALPEIYELNIGH+I+GRAVFDGLHKAVADMKAVMES 240
Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|YP_588729.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Baumannia cic
str. Hc (Homalodisca coagulata)]

gb|ABF13930.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Baumannia cicad

str. Hc (Homalodisca coagulata)]
Length=243

GENE ID: 4056676 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Baumannia cicadellinicola str. Hc (Homalodisca coagulata)]
(10 or fewer PubMed links)

Score = 352 bits (904), Expect = 1e-95, Method: Compositional matrix adjust.
Identities = 166/243 (68%), Positives = 201/243 (82%), Gaps = 0/243 (0%)

Query	1	MAELLGLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M+ LLL VNIDHIATLRNARGT +PDPVQAAAFIAE AGADGITVHLREDRRHI DRDV +	
Sbjct	1	MSRLLLNVDNIDHIATLRNARGTTWDPVQAAAFIAEDAGADGITVHLREDRRRHINDRDVTM	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC	120
		LRQT+ TRMNLEMA+T++M+AIA +P CCLVPEKROE+TTEGGGLDVA Q+ K+ +A	
Sbjct	61	LRQTIKTRMNLEMAITDDMIAIACSVRPDLCLVPEKROELTTEGGGLDVAQQKKKISNAI	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		L++AGI VSLFIDAD++QI+AAAE+G+P+IEIHTGICYA+A+ + E EL RI +AA	
Sbjct	121	YLLSEAGIMVSLFIDADKQQIEAAAEIGSPYIEIHTGICYANARNNTECIAELERIRQAAD	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A SLGLKVNAGHGLTYHNV+ IA + +HELNIGH+II RA+++GL A+ M L+	
Sbjct	181	YATSLGLKVNAGHGLTYHNVQDIAMLSFIHELNIGHSSIISRAIISGLNQAIINMINLLHN	240
Query	241	ARG 243	
		AR	
Sbjct	241	ARS 243	

>ref|ZP_01220096.1| pyridoxal phosphate biosynthetic protein [Photobacterium pro 3TCK]
gb|EAS43446.1| pyridoxal phosphate biosynthetic protein [Photobacterium profund 3TCK]
Length=243

Score = 352 bits (902), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLGLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M +LLGVNIDHIATLRNARGT YPDPV AA +AE+AGADGITVHLREDRRHI DRDVRI	
Sbjct	1	MNNILLGVNIDHIATLRNARGTRYDPVHAAEVAERAGADGITVHLREDRRRHINDRDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC	120
		L++T+ TRMNLEMAVT+EM++IA++TKP F CLVPEKR+E+TTEGGGLDVAGQ +K++ A	
Sbjct	61	LKETIQTRMNLEMAVTDEMVSIALDTKPEFVCLVPEKREELTTEGGGLDVAGQLEKIKAAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		++L AGI+VSLFIDAD QI A GAPF+E+HTG YADA+T+ Q EL +IA AAT	
Sbjct	121	QKLTAAGIKVSLFIDADRAQIDATLACGAPFVELHTGHYADAETEEAQQAEQELDKIASAAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A LG+KVNAGHGLTYHNVK IAA+PE++ELNIGH+IIIGRA GL AVA+MK +L+	
Sbjct	181	YAHGLGIKVNAGHGLTYHNVKPIAALPELYELNIGHSSIIGRAAFDGLNKAVADMKVEVLD	240
Query	241	AR 242	
		AR	
Sbjct	241	AR 242	

>ref|YP_002263870.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Aliivibrio LFI1238]

emb|CAQ80206.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Aliivibrio sal LFI1238]
Length=243

GENE ID: 6988220 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ
[Vibrio salmonicida LFI1238]

Score = 352 bits (902), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLGLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M+ +LLGVNIDH+ATLRNARGT YPDPV AA IAE+AGA GIT+HLREDRRHI DRDVRI	
Sbjct	1	MSSILLGVNIDHVATLRNARGTKYPDPVHAAEIAERAGAAGITIHLEDRRRHIKORDVRI	60
Query	61	LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC	120

```

Sbjct 61 LR+TL TRMNLEMAVT+EM+ IA+ET+P F CLVPEKR+E+TTEGGL+V GQ +K++ A
LRETlQTRMNLEMAVTDEMVGIALETQPEFVCLVPEKREELTTEGGLNVVGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIKAAT 180
+ L+ AGI+VSLFIDAD QI AA GAPFIE+HTG YADA+T+ + EL +IA AT
Sbjct 121 QTLKAGIKVSLFIDADNAQIDAACVACGAPFIELHTGAYADAETEEAEQIELKKIAAGAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AAS GL VNAGHGLTYHNV+AIAA+PE++ELNIGH+I+GRAV GL+ AVA+M R+ML
Sbjct 181 YAASKGLIVNAGHGLTYHNVKAIIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240

Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|ZP_01236135.1| pyridoxal phosphate biosynthetic protein [Vibrio angustum S1
gb|EAS63814.1| pyridoxal phosphate biosynthetic protein [Vibrio angustum S14]
Length=243

Score = 352 bits (902), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 168/243 (69%), Positives = 207/243 (85%), Gaps = 0/243 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRRHITDRDVRI 60
M +LLGVNIDHIATLRNARGT YDPV AA +AE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MNNILLGVNIDHIATLRNARGTRYDPVHAAEVAERAGADGITIHLREDRRRHINDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
LR+T+ TRMNLEMAVT+EM+AIA++ KP + CLVPEKR+E+TTEGGLDVAGQ +K++ A
Sbjct 61 LRETIQTRMNLEMAVTDEMVAIALDVKPEYVCLVPEKREELTTEGGLDVAGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIKAAT 180
++L AGI+VSLFIDAD QI AA GAPFIE+HTG YA+A T+ Q+ EL ++A A+
Sbjct 121 EKLTAAGIKVSLFIDADRAQIDAACGAPFIELHTGQYAEATTEEAQSDDELKKVAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A +LG+KVNAGHGLTYHNVK IAA+PE++ELNIGH+I+GRA+ GL+ +VA+M+ LM E
Sbjct 181 YAHNLGIKVNAGHGLTYHNVKPIAALPELYELNIGHSIMGRAMFDGLEKSVADMRLLMQE 240

Query 241 ARG 243
ARG
Sbjct 241 ARG 243

```

>gb|EED26525.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio parahaemol
16]
Length=243

Score = 351 bits (901), Expect = 2e-95, Method: Compositional matrix adjust.
Identities = 169/242 (69%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRRHITDRDVRI 60
M+ + LGVNIDHIATLRNARGT YDPV AA +AE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEVAERAGADGITIHLREDRRRHINDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
LR+T+ TRMNLEMAVT+EM+ IA+ T+P + CLVPEKR+E+TTEGGLDV GQ +K++ A
Sbjct 61 LRETIQTRMNLEMAVTDEMVEIALNTQPEYVCLVPEKREELTTEGGLDVVGQLEKVKAAAT 120


Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIKAAT 180
++L++AGI+VSLFIDAD EQI AA GAPFIE+HTG YADA+T+ +Q EL +IA A+
Sbjct 121 QKLSEAGIKVSLFIDADREQIDAACGAPFIELHTGHYADAETEEEDQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+AA LG+ VNAGHGLTYHNV AIAA+PE++ELNIGH+I+GRA GL AVA+MK M+
Sbjct 181 YAADLGITVNAGHGLTYHNVAAIAA+PELYELNIGHSIIGRAAFDGLHKAVADMKAQMVL 240

Query 241 AR 242
AR
Sbjct 241 AR 242

```

>ref|ZP_01988133.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio harvey
HY01]

ref|YP_001446696.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio har
ATCC BAA-1116]

gb|EDL67174.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio harveyi
HY01]

gb|ABU72469.1| **G** hypothetical protein VIBHAR_03533 [Vibrio harveyi ATCC BAA-111 Length=243]

Score = 350 bits (899), Expect = 4e-95, Method: Compositional matrix adjust.
Identities = 168/242 (69%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ + LGVNIDHIATLRNARGT YDPDV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1  MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHILDRDVRI 60

Query 61  LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC 120
          LR+T+ TRMNLEMAVT+EM+ IA++TKP F CLVPEKR+E+TTEGGGLDV GQ +K++ A
Sbjct 61  LRETIQTRMNLEMAVTDEMVEIALQTKPEFVCLVPEKREELTTEGGGLDVVGQLEKVKAAAT 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT 180
          ++L +AGI+VSLFIDAD +QI AA GAP+IE+HTG YADA T+ +Q EL +IA A+
Sbjct 121  QKLTEAGIKVSLFIDADRQQIDAACACGAPYIELHTGHYADATTEEDQQDELKKIAAGAS 180

Query 181  FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL+ +VAEMK +M+
Sbjct 181  YADDLGIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLEKSVAEMKAIMVA 240

Query 241  AR 242
          AR
Sbjct 241  AR 242

```

>**ref|ZP_01215567.1|** pyridoxal phosphate biosynthetic protein [Psychromonas sp. C
gb|EAS39633.1| pyridoxal phosphate biosynthetic protein [Psychromonas sp. CNPT3 Length=246]

Score = 350 bits (899), Expect = 5e-95, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 197/242 (81%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M++LLLGVNIDH+ATLRNARGT YP+P A IAE +GADGIT+HLREDRRHI DRDV I
Sbjct 1  MSKLLLGVNIDHVATLRNARGTCYPEPAHLAETSGADGITIHLREDRRHIIDRDVAI 60

Query 61  LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC 120
          L QTL TRMNLEMA+T+EM+ IA++TKP F CLVPEKR E+TTEGGGLDVAG DK R A
Sbjct 61  LAQTLQTRMNLEMAITDEMIDIAIKTKPAFVCLVPEKRAELTTEGGGLDVAGALDKTRSAV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT 180
          +RL AGIQVSLFIDAD+ QI AA GAP+IE+HTG YADA D QA EL R+A AT
Sbjct 121  QRLTQAGIQVSLFIDADKNQIDAALASGAPYIELHTGKYADALDDMQALELQRVASMAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LGLKVNAGHGL YHNVKAI A+PE+ ELNIGHAI I RA++ GL AV EMKRLM+E
Sbjct 181  YAHGLGLKVNAGHGLNYHNVKAI AALPEI IELNIGHAI IARALVDGLSVAVQEMKRLMIE 240

Query 241  AR 242
          R
Sbjct 241  GR 242

```

>**ref|ZP_01064680.1|** pyridoxal phosphate biosynthetic protein [Vibrio sp. MED222]
ref|YP_002418187.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Vibrio spl LGP32]
gb|EAQ53969.1| pyridoxal phosphate biosynthetic protein [Vibrio sp. MED222]
emb|CAV19823.1| **G** Pyridoxal phosphate biosynthetic protein pdxJ [Vibrio splendi LGP32]
Length=245

Score = 349 bits (895), Expect = 1e-94, Method: Compositional matrix adjust.
Identities = 169/242 (69%), Positives = 202/242 (83%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLRNARGT YDPDV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1  MSSILLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHIVDRDVRI 60

Query 61  LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKROEVTTEGGGLDVAGQORDKMRDAC 120
          L +T+ TRMNLEMAVT+EM+ IA++T P F CLVPEKR+E+TTEGGGLDV GQ +K++ A
Sbjct 61  LAETIQTRMNLEMAVTDEMVAIALDTNPEFVCLVPEKREELTTEGGGLDVVGQLEKIKAAAT 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAAKAAT 180
          ++L+ AGI+VSLFIDAD EQI AA GAPFIE+HTG YADAKT+ +Q EL +IA A+
Sbjct 121  EKLSAAGIKVSLFIDADREQIDAACACGAPFIELHTGHYADAKTEEDQQDELKKIAAGAS 180

```

```

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+I+GRAV GL AVA+MK +M
Sbjct 181 YADDLGITVNAGHGLTYHNVAPIAALPEIYELNIGHSIMGRAVFDGLNKAVADMKAVMET 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>gb|EAZ49556.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae V51]
Length=243

Score = 348 bits (893), Expect = 2e-94, Method: Compositional matrix adjust.
Identities = 172/242 (71%), Positives = 206/242 (85%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ + LGVNIDH+ATLRNARGT+YPDPV AA IAE+AGADGIT+HLREDRRHITDRDVRI
Sbjct 1 MSSIYLGVNIDHVATLRNARGTSYPDPVHAAEIAERAGADGITIHLREDRRHITDRDVRI 60



Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDV GQ ++++ A
Sbjct 61 LRETLQTRMNLEMAVTDDEMVEIALQTQPEYVCLVPEKREELTTEGGLDVLGQLERVKAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA
Sbjct 121 EKLTAAGIKVSLFIDADREQIDAAKACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAA 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV AIAAIP++ELNIGHAIIGRAV GL AVA+MK +M+
Sbjct 181 YAHDLGITVNAGHGLTYHNVAAIAAIPDIYELNIGHAIIGRAVFDGLAKAVADMKAIMVA 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|NP_798948.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio parahaemolyticus RIMD 2210633]
sp|Q87LP2.1|PDXJ VIBPA RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
dbj|BAC60832.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio parahaemolyticus RIMD 2210633]
Length=243

GENE ID: 1190093 VP2569 | pyridoxal phosphate biosynthetic protein PdxJ
[Vibrio parahaemolyticus RIMD 2210633] (10 or fewer PubMed links)

Score = 348 bits (892), Expect = 3e-94, Method: Compositional matrix adjust.
Identities = 173/242 (71%), Positives = 207/242 (85%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHITDRDVRI
Sbjct 1 MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRHITDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC 120
          LR+T+ TRMNLEMAVTEEM+ IA++TKP F CLVPEKR+E+TTEGGLDV GQ DK++ A
Sbjct 61 LRETIQTRMNLEMAVTEEMVEIALKTKPEFVCLVPEKREELTTEGGLDVVGQLDKVKAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L +AGI+VSLFIDAD +QI+AA + GAPFIE+HTG YADA+T+ EQ EL +IA A+
Sbjct 121 QKLTEAGIKVSLFIDADRQQIEAAKQCGAPFIELHTGHYADAETEEQQAELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL+ +VAEMK LM+
Sbjct 181 YADDLGIIVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLEKSVAEMKALMIA 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_00991369.1| pyridoxal phosphate biosynthetic protein [Vibrio splendidus]
gb|EAP93636.1| pyridoxal phosphate biosynthetic protein [Vibrio splendidus 12B0]
Length=245

Score = 347 bits (890), Expect = 4e-94, Method: Compositional matrix adjust.
Identities = 168/242 (69%), Positives = 202/242 (83%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRRHITDRDVRI 60
Sbjct 1  MSSILLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRRHIVDRDVRI 60


Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQEVTTTEGGGLDVAGQDKMRDAC 120
Sbjct 61  LAETIQTRMNLEMAVTDEMVMQIALDTNPEFVCLVPEKREELTTEGGGLDVVGQLEKIKAAAT 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
Sbjct 121  EKLSAAGIKVSLFIDAEREQIDAAKACGAPFIELHTGHYADAKTEEDQQDELKKIAAGAS 180


Query 181  FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
Sbjct 181  YADDLGITVNAGHGLTYHNVAPIAALPEIYELNIGHSIMGRAVFDGLNKAVADMKAVMET 240


Query 241  AR 242
Sbjct 241  AR 242


```


>ref|NP_232087.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O1 biovar eltor str. N16961]
 ref|ZP_01678308.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 2740-80]
 ref|ZP_01953186.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MAK 757]
 15 more sequence titles

ref|ZP_01957675.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-3]
 ref|ZP_01979577.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-2]
 ref|ZP_01983536.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 623-39]

ref|YP_002066631.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae M010]

ref|YP_002069749.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae RC385]

ref|YP_002174421.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae AM-19226]

sp|Q9KPB5.1|PDXJ VIBCH RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
 gb|AAF95600.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O1 biovar El Tor str. N16961]


gb|EAX57295.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 2740-80]


gb|EAY37632.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MAK 757]

gb|EAY40114.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-3]

gb|EDL71773.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae 623-39]

gb|EDM53535.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae MZO-2]

gb|EDN11667.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae RC385]

gb|EDN14389.1|  pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae AM-19226]
 Length=243

GENE ID: 2613000 VC2458 | pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae O1 biovar eltor str. N16961] (10 or fewer PubMed links)

Score = 347 bits (890), Expect = 5e-94, Method: Compositional matrix adjust.
 Identities = 172/242 (71%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRRHITDRDVRI 60
Sbjct 1  MSSIYLGVNIDHVATLRNARGTQYPDPVHAAEIAERAGADGITIHLREDRRRHITDRDVRI 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKQEVTTTEGGGLDVAGQDKMRDAC 120
Sbjct 61  LRETLOTRMNLEMAVTDEMVEIALQTQPEYVCLVPEKREELTTEGGGLDVLGQLERVKAAT 120

```

```

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA
Sbjct 121 EKLTAAGIKVSLFIDADREQIDAAKACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAA 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV AIAAIP++ELNIGHAIIGRAV GL AVA+MK +M+
Sbjct 181 YAHDLGITVNAGHGLTYHNVAAIAAIPAIYELNIGHAIIGRAVFDGLAKAVADMKAIMVA 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_02196848.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio campbe
AND4]
gb|EDP58079.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio campbellii
AND4]
Length=243

Score = 347 bits (889), Expect = 6e-94, Method: Compositional matrix adjust.
Identities = 166/242 (68%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+ + LGVNIDHIATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRHI DRDVRI
Sbjct 1 MSSIYLGVNIDHIATLRNARGTKYPDPVHAAEIAERAGADGITIHLREDRRRHILDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
          LR+T+ TRMNLEMAVT+EM+ IA++T+P F CLVPEKR+E+TTEGGGLDVAGQ +K++ A
Sbjct 61 LRETIQTRMNLEMAVTDEMVEIALKTQPEFVCLVPEKREELTTEGGGLDVAGQLEKVKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          +L +AGI+VSLFIDAD +QI AA GAP++E+HTG YADA T+ +Q EL +IA A+
Sbjct 121 HKLTEAGIKVSLFIDADRQQIDAAKACGAPYVELHTGHYADATTEEDQQDELKKIAAGAS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV IAA+PE++ELNIGH+IIGRAV GL+ +VA+MK +M+
Sbjct 181 YADDLGITVNAGHGLTYHNVAPIAALPEIYELNIGHSIIGRAVFDGLEKSVADMKAIMVA 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_01681976.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholera
V52]
ref|YP_001217960.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cho
O395]
gb|EAX61205.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae
V52]
gb|ABQ21999.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae
O395]
Length=243

Score = 347 bits (889), Expect = 7e-94, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 205/242 (84%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+ + LGVNIDH+ATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRRHITDRDVRI
Sbjct 1 MSSIYLGVNIDHVATLRNARGTQYPDPVHAAEIAERAGADGITIHLREDRRRHITDRDVRI 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
          LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGGLDV GQ ++++ A
Sbjct 61 LRETLQTRMNLEMAVTDEMVEIALQTQPEYVCLVPEKREELTTEGGGLDVGLQLERVKAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          ++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA
Sbjct 121 EKLTAAGIKVSLFIDADREQIDAAKACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAA 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A LG+ VNAGHGLTYHNV AIAAIP++ELNIGHAIIGRAV GL AV++MK +M+
Sbjct 181 YAHDLGITVNAGHGLTYHNVAAIAAIPAIYELNIGHAIIGRAVFDGLAKAVSDMKAIQMV 240

Query 241 AR 242
          AR
Sbjct 241 AR 242

```

>ref|ZP_01949430.1| pyridoxal phosphate biosynthetic protein PdxJ [Vibrio cholerae
V52]

1587]
gb|EAY34143.1| pyridoxal phosphate biosynthetic protein PdxJ [*Vibrio cholerae*
 1587]
 Length=243

Score = 345 bits (886), Expect = 1e-93, Method: Compositional matrix adjust.
 Identities = 171/242 (70%), Positives = 204/242 (84%), Gaps = 0/242 (0%)

Query	1	MAELLGLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M+ + LGVNIDH+ATLRNARGT YPDPV AA IAE+AGADGIT+HLREDRRRHITDRDVRI	
Sbjct	1	MSSIYLGVNIDHVATLRNARGTQYPDPVHAAEIAERAGADGITIHLREDRRRHITDRDVRI	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		LR+TL TRMNLEMAVT+EM+ IA++T+P + CLVPEKR+E+TTEGGLDV GQ ++++ A	
Sbjct	61	LRET LQTRMNLEMAVTDEMVEIALQTQPEYVCLVPEKREELTTEGGLDVLGQLERVKAAT	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
		++L AGI+VSLFIDAD EQI AA GAPFIE+HTG Y+DAK+D +Q EL +IA AA	
Sbjct	121	EKLTAAGIKVSLFIDADREQIDAACACGAPFIELHTGHYSDAKSDVDQQNELKKIAAAAA	180
Query	181	FAASLGLKVNAGHGLTYHNVAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A G+ VNAGHGLTYHNVAIAAIP+ELNIGHAIIGRAV GL AVA+MK +M+	
Sbjct	181	YAHDFGITVNAGHGLTYHNVAIAAIP+ELNIGHAIIGRAVFDGLAKAVADMKAIMVA	240
Query	241	AR	242
		AR	
Sbjct	241	AR	242

>**ref|YP_663265.1|** **G** pyridoxal phosphate biosynthetic protein PdxJ [*Pseudoalteromonas atlantica* T6c]

gb|ABG42211.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [*Pseudoalteromonas atlantica* T6c]
 Length=245

GENE ID: 4175489 Pat1_3709 | pyridoxal phosphate biosynthetic protein PdxJ [*Pseudoalteromonas atlantica* T6c]

Score = 345 bits (885), Expect = 2e-93, Method: Compositional matrix adjust.
 Identities = 169/243 (69%), Positives = 200/243 (82%), Gaps = 0/243 (0%)

Query	1	MAELLGLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI	60
		M ++LLGVNIDHIATLRNARGT+YPDPV AA IAE+AGADGIT+HLREDRRRHITDRDV +	
Sbjct	1	MRDILLGVNIDHIATLRNARGTSYPDPVHAADIAERAGADGITIHLREDRRRHIMDRDVAL	60
Query	61	LRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDAC	120
		LRQT++TR+NLEMAVT+EM+ IA+ T+P FCCLVPEKR+E+TTEGGLDV G + K+ DAC	
Sbjct	61	LRQTLNTRNLNLEMAVTDEMVEIALNTQPEFCCLVPEKREELTTEGGLDVVGNNQKQIADAC	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT	180
		K+L+DAGI VSLFIDAD QI AA AP+IEIHTG YA+AK +AEQ ELA++	
Sbjct	121	KQLSDAGILVSLFIDADFAQIDAACVACNAPYIEIHTGQYAEAKNEAEQAEALAKLVAGIE	180
Query	181	FAASLGLKVNAGHGLTYHNVAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A + GLKVNAGHGLTYHNVAIAAIP+ELNIGHAIIGRAV GL AV++M+ LMLE	
Sbjct	181	YADAKGLKVNAGHGLTYHNVAIAAIP+ELNIGHAIIGRAVFDGLKAVSDMRSLMLE	240
Query	241	ARG	243
		AR	
Sbjct	241	ARS	243

>**ref|ZP_03354955.1|** pyridoxal phosphate biosynthetic protein PdxJ [*Salmonella enterica* serovar Typhi str. E01-6750]
 Length=184

Score = 343 bits (881), Expect = 6e-93, Method: Compositional matrix adjust.
 Identities = 169/184 (91%), Positives = 176/184 (95%), Gaps = 0/184 (0%)

Query	60	ILRQTL DTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDA	119
		+LRQTL TRMNLEMAVTEEMLAIAVET+PHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDA	
Sbjct	1	MLRQTLHTRMNLEMAVTEEMLAIAVETRPHFCCLVPEKRQEVTTTEGGLDVAGQORDKMRDA	60
Query	120	CKRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAA	179
		C RLA AGIQVSLFIDADE QI AAAEVGGAPFIEIHTGCIY+A+TDAEQA+ELARIA AA	
Sbjct	61	CARLAAAGIQVSLFIDADERQINAAAEVGGAPFIEIHTGCIYANAETDAEQAKELARIASAA	120
Query	180	TFAASLGLKVNAGHGLTYHNVAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLML	239

```

Sbjct 121 T AA LGLKVNAGHGLTYHNVKAI AA+PEMHENLIGHAIIGRAVMTGLK+AVAEMKRLML 180
          TLAARLGLKVNAGHGLTYHNVKAI AALPEMHENLIGHAIIGRAVMTGLKEAVAEMKRLML
Query 240 EARG 243
          EARG
Sbjct 181 EARG 184

```

>ref|ZP_01898798.1| pyridoxal phosphate biosynthetic protein [Moritella sp. PE36
gb|EDM66702.1| pyridoxal phosphate biosynthetic protein [Moritella sp. PE36]
Length=245

Score = 343 bits (880), Expect = 7e-93, Method: Compositional matrix adjust.
Identities = 167/242 (69%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
        M ++ LGVNIDHIATLR ARG T YDPV AA +AE GADGITVHLREDRRHI DRDV R+
Sbjct 1 MNKIFLGVNIDHIATLRQARGTTYDPVHAAVAELNGADGITVHLREDRRHIQDRDVRV 60

Query 61 LRQTL DTRMNLEMAVTEEM LAIAVETKPHFCCLVPEKRQEV TTEGGLDVAGQ RDKMRDAC 120
        L++T+ TRMNLEMAVT EML IA E KP F CLVPEKR+E+TTEGGLDV GQ+DK+ A
Sbjct 61 LKETIQTRMNLEMAVTAEMLDIACEIKPEFVCLVPEKREELTTEGGLDVLGQQDKITQAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEV GAFP FIEIHTG CYADAKTDAEQ AQELARIAKAAT 180
        KRL++AGI VSLFIDAD+EQI AA GAP+IE+HTG YADA+++ EQ EL +IA +
Sbjct 121 KRLSEAGILVSLFIDADKEQIDA AVASGAPYIEVHTGAYADA ESEGEQQ AELKKIAAGVS 180

Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
        +A + GLKVNAGHGL YHNV+ IAAIPE++ELNIGHAI I RA GL AV +M+ +M E
Sbjct 181 YAHNAGLKVNAGHGLHYHNVQPIAAIPEIYELNIGHAI IARA AFDGLGKAVKDMQVIMQE 240

Query 241 AR 242
        AR
Sbjct 241 AR 242

```

>ref|ZP_03347562.1| pyridoxal phosphate biosynthetic protein PdxJ [Salmonella en
subsp. enterica serovar Typhi str. E00-7866]
Length=179

Score = 340 bits (872), Expect = 6e-92, Method: Compositional matrix adjust.
Identities = 168/179 (93%), Positives = 172/179 (96%), Gaps = 0/179 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
        MAELLLGVNIDHIATLRNARGT YDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI
Sbjct 1 MAELLLGVNIDHIATLRNARGTDYDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60

Query 61 LRQTL DTRMNLEMAVTEEM LAIAVETKPHFCCLVPEKRQEV TTEGGLDVAGQ RDKMRDAC 120
        LRQTL TRMNLEMAVTEEM LAIAVET+PHFCCLVPEKRQEV TTEGGLDVAGQ RDKMRDAC
Sbjct 61 LRQTLHTRMNLEMAVTEEM LAIAVETRPHFCCLVPEKRQEV TTEGGLDVAGQ RDKMRDAC 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEV GAFP FIEIHTG CYADAKTDAEQ AQELARIAKAA 179
        RLA AGIQVSLFIDADE QI AAAEV GAFP FIEIHTG CYA+A+TDAEQ A+ELARIA AA
Sbjct 121 ARLAAAGIQVSLFIDADERQINAAAEV GAFP FIEIHTG CYANAETDAEQ AKELARIASAA 179

```

>ref|ZP_01614216.1| pyridoxal phosphate biosynthetic protein [Alteromonadales ba
TW-7]
gb|EAW26571.1| pyridoxal phosphate biosynthetic protein [Alteromonadales bacter
TW-7]
Length=243

Score = 339 bits (869), Expect = 1e-91, Method: Compositional matrix adjust.
Identities = 162/242 (66%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFI AEQAGADGITVHLREDRRHITDRDVRI 60
        M ++LLGVN+DHIATLR ARG T YDPV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MKDILLGVNV DHIATLRQARGTTYDP PAHAASVAEHAGADGITIHLREDRRHIQDRDVYV 60

Query 61 LRQTL DTRMNLEMAVTEEM LAIAVETKPHFCCLVPEKRQEV TTEGGLDVAGQ RDKMRDAC 120
        + +T+ TRMNLE AVT+EM+AIA+E KP + CLVPEKR+E+TTEGGLDVAG +K++ A
Sbjct 61 MAKTIQTRMNLETAVTDEMI AIALEV KPEYVCLVPEKREELTTEGGLDVAGNIEKIKAAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEV GAFP FIEIHTG CYADAKTDAEQ AQELARIAKAAT 180
        K L DAGI+VSLFIDAD Q+ AA GAP++EIHTG YADA D++ ++EL I +
Sbjct 121 KTLTDAGIKVSLFIDADTAQLDAAKACGAPYVEIHTGAYADATNDS DLSKELEHIRQGVQ 180

Query 181 FAASLGLKVNAGHGLTYHNVKAI AAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
        +AASLGL VNAGHGL YHNVK IAA+PE++ELNIGHAI I RA + GL AV +MKRLM+E
Sbjct 181 YAASLGLIVNAGHGLNYHNVKPIAAMPEIYELNIGHAI IARA AIDGLDKAVRDMKRLMIE 240

```

Query 241 AR 242
 AR
 Sbjct 241 AR 242

>ref|ZP_01450587.1| pyridoxal phosphate biosynthetic protein [alpha proteobacter HTCC2255]
 ref|ZP_03561535.1| pyridoxine 5'-phosphate synthase [Glaciecola sp. HTCC2999]
 Length=254

Score = 338 bits (866), Expect = 3e-91, Method: Compositional matrix adjust.
 Identities = 168/240 (70%), Positives = 196/240 (81%), Gaps = 0/240 (0%)

Query 3 ELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRILR 62
 E+LLGVNIDH+ATLRNARGT+YPDPV AA IAE+AGADGITVHLREDRRHI DRDV IL
 Sbjct 6 EVLLGVNIDHVATLRNARGTSYPDPVHAADIAERAGADGITVHLREDRRRHINDRDVEILA 65

Query 63 QTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQRDKMRDACKR 122
 +TL+TRMNLEMAVT+EMLAIA +T+P FCCLVPEKR E+TTEGGL+VAG +M+DAC +
 Sbjct 66 RTLNTRMNLEMAVTDEMLAIAKKTQPAFCCLVPEKRAELTTEGGLNVAGNLSRMQDACGQ 125

Query 123 LADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAATFA 182
 LA+ GI VSLFIDA+ EQI AA P+IEIHTG YADA + +Q QELA++ FA
 Sbjct 126 LAEQGILVSLFIDAEPEQIDAACVADVPYIEIHTGQYADATSIKQQTQELAKLKAGIQFA 185

Query 183 ASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEAR 242
 GL+VNAGHGL YHNVK IAAIPE+ ELNIGHAI+ RA+ GL AV++M+ LM EAR
 Sbjct 186 HQRGLQVNAGHGLHYHNVKPIAAIPEIVELNIGHAIMARAMFDGLGKAVSDMRALMQEAR 245

>ref|YP_563765.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella de OS217]

gb|ABE56042.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella deni OS217]
 Length=245

GENE ID: 4019282 Sden_2763 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella denitrificans OS217]

Score = 335 bits (860), Expect = 1e-90, Method: Compositional matrix adjust.
 Identities = 174/242 (71%), Positives = 197/242 (81%), Gaps = 0/242 (0%)

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
 M+ +LLG+NIDHIATLR ARG T YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
 Sbjct 1 MSGILLGINIDHIATLRQARGTNYDPVHAAVAEHAGADGITIHLREDRRRHIIIDRDVYL 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQRDKMRDAC 120
 L +TL TRMN E AVTEEM+AIA + KP + CLVPEKR+E+TTEGGLDVAGQ DK+ A
 Sbjct 61 LAKTLKTRMNFEEFAVTEEMIAIACDVKPAYACLVPEKREELTTEGGLDVAGQMDKITA AV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
 RLA GI+VSLFIDAD QI AA GAP+IEIHTGICYADAK D+EQ A EL RI K A
 Sbjct 121 SRLAAHGIKVSLFIDADATQIDA AVATGAPYIEIHTGICYADAKNDSEQAMELERITKMAK 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
 +A S GL VNAGHGL YHNVKAIAAIP E++ELNIGHA+I RA + GL+ AV +MKRLMLE
 Sbjct 181 YAHSGKLVVNAGHGLHYHNVKAIAAIP ELYELNIGHAVIARA AIDGLETAVRDMKRLMLE 240

Query 241 AR 242
 R
 Sbjct 241 GR 242

>ref|YP_001553716.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS195]

gb|ABX48456.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella balt OS195]
 Length=245

GENE ID: 5753009 Sbal195_1281 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS195]

Score = 335 bits (859), Expect = 2e-90, Method: Compositional matrix adjust.
 Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60

```

Sbjct 1      M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
MSRILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL 60

Query 61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQDKMRDAC 120
L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGGLDVAGQ DK+ A
Sbjct 61      LAKTLKTRMNFECVTEEMLNIAACEIKPTYVCLVPEKRQEVTTTEGGGLDVAGQLDKITSV 120

Query 121     KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIKAAT 180
RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+AE+A ELARI++ A
Sbjct 121     TRLAATEGIQVSLFIDADKTQIDAASVAGAPLIEIHTGCIYADAKTEAEEATELARISEMAK 180

Query 181     FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181     YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLMLLE 240

Query 241     AR 242
R
Sbjct 241     GR 242

```

>ref|YP_270774.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Colwellia psy 34H]

sp|Q47WP8.1|PDXJ COLP3 **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short= gb|AAZ25393.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Colwellia psych 34H]
Length=246

GENE ID: 3519304 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Colwellia psychrerythraea 34H] (10 or fewer PubMed links)

Score = 335 bits (859), Expect = 2e-90, Method: Compositional matrix adjust.
Identities = 167/242 (69%), Positives = 192/242 (79%), Gaps = 0/242 (0%)

```

Query 1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
M+ELLLGVN+DHIATLR ARG+YPDPV AA +AE AGADGITVHLREDRRHI DRD+ +
Sbjct 1      MSELLLLGVNVNDHIATLRQARGTNYDPVYAASVAEHAGADGITVHLREDRRHIQDRDIHV 60

Query 61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQDKMRDAC 120
L+QTL TRMN EMV+EM+AIA + KP FCCLVPEKR+E+TTEGGGLDV GQ DK+ A
Sbjct 61      LKQTLHTRMNFEMAVTDEMIAIACDVKPVFCCLVPEKREELTTEGGGLDVVGQLDKITKAT 120

Query 121     KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIKAAT 180
++L AGI VSLFIDAD+ QI AA AP+IEIHTG YAD ++ EQ EL R+
Sbjct 121     EQLTAAGIAVSLFIDADKAQIDAASVASKAPYIEIHTGHIYADLSSEEEQLIELERLTVGIK 180

Query 181     FAASLGLKVNAGHGLTYHNVKAAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
+A +LGLKVNAGHGL Y NVK IAAI E+ ELNIGHAI RA + GL AV +MK+LMLE
Sbjct 181     YAHNLGLKVNAGHGLNYFNVKPIAAIKEIIELNIGHAIIARAAIDGLDKAVRDMKQLMLE 240

Query 241     AR 242
AR
Sbjct 241     AR 242

```

>ref|YP_734973.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp MR-4]

gb|ABI39916.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-4]
Length=245

GENE ID: 4253416 **Shewmr4_2845** | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-4]

Score = 335 bits (858), Expect = 3e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1      MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI 60
M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1      MSRILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL 60

Query 61      LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQDKMRDAC 120
L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGGLDVAGQ DK+ A
Sbjct 61      LAKTLKTRMNFECVTEEMLNIACEVKTPTVCLVPEKRQEVTTTEGGGLDVAGQLDKITA 120

Query 121     KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIKAAT 180
RLA GIQVSLFIDAD+ QI AA E GAP IEIHTGCIYADAKT E+A+ELARI++ A

```



```

Sbjct 121 SRLAANGIQVSLFIDADKTQIDAAVESGAPLIEIHTGCIYADAKTAESEAKELARISEMAK 180
Query 181 FAASLGLKVNAGHGLTYHNVKAIIPPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181 YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE 240
Query 241 AR 242
      R
Sbjct 241 GR 242

```

>ref|YP_339261.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Pseudoalteromonas haloplanktis TAC125]

sp|Q3IDK9.1|PDXJ PSEHT **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=emb|CAI85818.1| **G** pyridoxine 5'-phosphate (PNP) synthase [Pseudoalteromonas haloplanktis TAC125]
Length=243

• GENE ID: 3709965 **pdxJ** | pyridoxal phosphate biosynthetic protein PdxJ [Pseudoalteromonas haloplanktis TAC125] (10 or fewer PubMed links)

Score = 334 bits (856), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 161/242 (66%), Positives = 195/242 (80%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRRHITDRDVRI 60
      M ++LLGVN+DHIATLR ARG+YPDP AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MKDILLGVNVDHIATLRQARGTSYPDPAHAASVAEHAGADGITIHLREDRRHIQDRDVYV 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDRDKMRDAC 120
      + +T+ TRMNLE AVT+EM+ IA+E KP + CLVPEKR+E+TTEGGLDVAG +K+ A
Sbjct 61 MAKTIQTRMNLETAVTDEMINIALEVKPEYVCLVPEKREELTTEGGLDVAGNLEKITAAT 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      K L+DAGI+VSLFIDAD+ Q+ AA GAP++EIHTG YADA TD ++EL I +
Sbjct 121 KTLSDAGIKVSLFIDADKAQLDAAKATGAPYVEIHTGAYADATTDEAISKELEHIRQGVK 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +AAS+GL VNAGHGL YHNVK IAA+ E++ELNIGHAI RA + GL AV +MKRLMLE
Sbjct 181 YAASIGLIVNAGHGLHYHNVKPIAAEELIYELNIGHAIARAAIDGLDKAVRDMKRLMLE 240

Query 241 AR 242
      AR
Sbjct 241 AR 242

```

>ref|YP_002359017.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS223]

gb|ACK47594.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS223]
Length=245

GENE ID: 7087887 **Sba1223_3109** | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS223]

Score = 334 bits (856), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRRHITDRDVRI 60
      M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDRDKMRDAC 120
      L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A
Sbjct 61 LAKTLKTRMNFECVTEEMLNIAICEIKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITA AV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
      RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+AE+A ELARI++ A
Sbjct 121 TRLAAGIQVSLFIDADKTQIDAAVAAGAPLIEIHTGCIYADAKTEAESEATELARISEMAK 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIIPPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181 YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLMLLE 240

Query 241 AR 242
      R
Sbjct 241 GR 242

```

>ref|YP_001365462.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS185]

gb|ABS07399.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella balt OS185]
Length=245

GENE ID: 5372257 Shew185_1248 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella baltica OS185]

Score = 334 bits (856), Expect = 4e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRRH DRDV +
Sbjct 1  MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRRHIDRDVYL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIIVETKPHFCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A
Sbjct 61  LAKTLKTRMNFECVTEEMLNIACEIKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITA AV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+AE+A ELARI++ A
Sbjct 121  TRLAAEGIQVSLFIDADKTQIDA AVASGAPLIEIHTGCIYADAKTEAEAEELARISEMAK 180

Query 181  FAASLGLKVNAGHGLTYHNVKAI AAIPEMHEL NIGHAI IGRAVMTGLKDAVAEMKRLMLE 240
          +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181  YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLML E 240

Query 241  AR 242
          R
Sbjct 241  GR 242

```

>ref|YP_001182689.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella CN-32]

gb|ABP74890.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella putr CN-32]
Length=245

GENE ID: 5081572 Sputcn32_1162 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella putrefaciens CN-32]

Score = 333 bits (854), Expect = 8e-90, Method: Compositional matrix adjust.
Identities = 176/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRRHITDRDVRI 60
          M+ +LLGVNIDHIATLR ARG+YPDPV AA +AE AGADGIT+HLREDRRRH DRDV +
Sbjct 1  MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRRHIDRDVYL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIIVETKPHFCLVPEKRQEVTTTEGGLDVAGQDKMRDAC 120
          L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A
Sbjct 61  LAKTLKTRMNFECVTEEMLNIACEIKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITA AV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+AE+A ELARI++ A
Sbjct 121  TRLAAEGIQVSLFIDADKTQIDA AVASGAPLIEIHTGCIYADAKTEAEAEELARISEMAK 180

Query 181  FAASLGLKVNAGHGLTYHNVKAI AAIPEMHEL NIGHAI IGRAVMTGLKDAVAEMKRLMLE 240
          +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181  YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE 240

Query 241  AR 242
          R
Sbjct 241  GR 242

```

>ref|YP_001049591.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella OS155]

gb|ABN60722.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella balt OS155]
Length=245

GENE ID: 4842456 Sbal_1204 | pyridoxal phosphate biosynthetic protein PdxJ

[Shewanella baltica OS155]

Score = 333 bits (853), Expect = 8e-90, Method: Compositional matrix adjust.
 Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLR ARG+YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1  MSRIILLGVNIDHIATLRQARGTSYPDPVHAAAVAHAAGADGITIHLREDRRHIIDRDVYL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQDKMRDAC 120
          L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGGLDVAGQ DK+ A
Sbjct 61  LAKTLKTRMNFECVTEEMLNIAICEIKPTYVCLVPEKRQEVTTTEGGGLDVAGQLDKITAAY 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RLA GIQVSLFIDAD+ QI AA GAP IEIHTGCIYADAKT+A++A ELARI++ A
Sbjct 121  TRLAAGIQVSLFIDADKTQIDAASVAGAPLIEIHTGCIYADAKTEAQEATELARISEMAK 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL AV +MK LMLE
Sbjct 181  YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKVLMLLE 240

Query 241  AR 242
          R
Sbjct 241  GR 242

```

>ref|YP_001500902.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella ATCC 700345]

gb|ABV86367.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella peal ATCC 700345]
 Length=245

GENE ID: 5661439 Spea 1040 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella pealeana ATCC 700345]

Score = 332 bits (852), Expect = 1e-89, Method: Compositional matrix adjust.
 Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLR ARG+YDPDV AA +AE AGA+GIT+HLREDRRHI DRDV
Sbjct 1  MSRIILLGVNIDHIATLRQARGTNYPDPVHAAAVAHAAGAEGITIHLREDRRHIIDRDVYT 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQDKMRDAC 120
          L +TL TRMN EMVTEEML IA E KP + CLVPEKR+E+TTEGGGLDVAGQ+DK+ A
Sbjct 61  LAKTLKTRMNFEMVTEEMLNIAICEIKPAYVCLVPEKREELTTEGGGLDVAGQQDKIAAAV 120

Query 121  KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGCIYADAKTDAEQAQELARIAKAAT 180
          RL GI+VSLFIDAD QI AA VGAP IEIHTGCIYADA+TD+EQA EL RI + AT
Sbjct 121  ARLTKEGIKVSLFIDADSTQIDAASVAVGAPVIEIHTGCIYADAETDSEQAAELKRITEMAT 180

Query 181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
          +A GL VNAGHGL YHNVKAIAAIPE++ELNIGHAI RA + GL AV +MK+LMLE
Sbjct 181  YAHGKGLVVNAGHGLHYHNVKAIAAIPELYELNIGHAIARAAIDGLATAVRDMKQLMLE 240

Query 241  AR 242
          R
Sbjct 241  GR 242

```

>ref|YP_738968.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp MR-7]

gb|ABI43911.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-7]
 Length=245

GENE ID: 4257702 Shewmr7_2927 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. MR-7]

Score = 332 bits (851), Expect = 2e-89, Method: Compositional matrix adjust.
 Identities = 175/242 (72%), Positives = 195/242 (80%), Gaps = 0/242 (0%)

```

Query 1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
          M+ +LLGVNIDHIATLR ARG+YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1  MSRIILLGVNIDHIATLRQARGTSYPDPVHAAAVAHAAGADGITIHLREDRRHIIDRDVYL 60

Query 61  LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQDKMRDAC 120
          L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGGLDVAGQ DK+ A

```

```

Sbjct  61  LAKTLKTRMNFECVTEEMLNIAACEVKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITVAV  120
Query  121  KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT  180
          RLA  GIQVSLFIDAD+ QI AA  GAP IEIHTGCIYADAKT  E+A+ELARI++ A
Sbjct  121  SRLAANGIQVSLFIDADKTQIDAAVASGAPLIEIHTGCIYADAKTAEAAEAKELARISEMAK  180
Query  181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +A  GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL  AV +MK LMLE
Sbjct  181  YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE  240
Query  241  AR  242
          R
Sbjct  241  GR  242

```

>ref|YP_751604.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella fr NCIMB 400]

gb|ABI72765.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella frig NCIMB 400]
Length=265

GENE ID: 4279831 Sfri 2926 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella frigidimarina NCIMB 400]

Score = 332 bits (851), Expect = 2e-89, Method: Compositional matrix adjust.
Identities = 173/239 (72%), Positives = 196/239 (82%), Gaps = 0/239 (0%)

```

Query  4  LLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRILRQ  63
          +LLG+NIDHIATLR ARGV YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +L +
Sbjct  24  ILLGINIDHIATLRQARGTHYPDPVHAAVAEHAGADGITIHLREDRRHIQDRDVYLLAK  83
Query  64  TLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDACKRL  123
          TL TRMN E AVTEEM+AIA + KP + CLVPEKR+E+TTEGGLDVAGQ DK+R A  RL
Sbjct  84  TLKTRMNFECVTEEMIAIACDIKPAYACLVPEKREELTTEGGLDVAGQLDKIRSAVTRL  143
Query  124  ADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAATFAA  183
          A  GI+VSLFIDAD+ QI AA  GAP+IEIHTGCIYADA TDAEQA EL RI + A +A
Sbjct  144  AAEIGKVSFLFIDADKTQIDAAVLSGAPYIEIHTGCIYADAITDAEQADELVRITEMAQYAH  203
Query  184  SLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLEAR  242
          S GL VNAGHGL YHNVKAIAAIPE++ELNIGHA+I RA + GL  AV +MK+LMLE R
Sbjct  204  SKGLVVNAGHGLHYHNVKAIAAIPELYELNIGHAIVARAAIDGLDTAVRDMKKMLMEGR  262

```

>ref|YP_964373.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp W3-18-1]

ref|ZP_01706794.1| pyridoxal phosphate biosynthetic protein PdxJ [Shewanella pu 200]

gb|ABM25819.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. W3-18-1]

gb|EAY52920.1| pyridoxal phosphate biosynthetic protein PdxJ [Shewanella putref 200]
Length=245

GENE ID: 4661399 Sputw3181_3002 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. W3-18-1]

Score = 332 bits (850), Expect = 2e-89, Method: Compositional matrix adjust.
Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

```

Query  1  MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIQAGADGITVHLREDRRHITDRDVRI  60
          M+ +LLGVNIDHIATLR ARGV+YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct  1  MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGADGITIHLREDRRHIIDRDVYL  60
Query  61  LRQTLDTMNLMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQDKMRDAC  120
          L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGLDVAGQ DK+ A
Sbjct  61  LAKTLKTRMNFECVTEEMLNIACEIKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITAAV  120
Query  121  KRLADAGIQVSLFIDADEEQIKAAAEVGGAPFIEIHTGCIYADAKTDAEQAQELARIAKAAT  180
          RLA  GIQVSLFIDAD+ QI AA  GAP IEIHTGC+ADAKT+AE+A ELARI++ A
Sbjct  121  TRLAEEGIQVSLFIDADKTQIDAAVASGAPLIEIHTGCFADAKTEAAEAEIARISEMAK  180
Query  181  FAASLGLKVNAGHGLTYHNVKAIAAIPEMHENLIGHAIIGRAVMTGLKDAVAEMKRLMLE  240
          +A  GL VNAGHGL YHNVK IAAIPE++ELNIGHAI+ RA + GL  AV +MK LMLE
Sbjct  181  YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE  240
Query  241  AR  242

```

Sbjct 241 ^RGR 242

>ref|YP_001673314.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella HAW-EB4]

gb|ABZ75655.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella hali HAW-EB4]
Length=245

GENE ID: 5904608 Shal_1086 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella halifaxensis HAW-EB4]

Score = 330 bits (845), Expect = 7e-89, Method: Compositional matrix adjust.
Identities = 175/242 (72%), Positives = 196/242 (80%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M +LLGVNIDHIATLR ARG T YDPDV AA +AE AGA+GIT+HLREDRRHI DRDV	
Sbjct	1	MGRILLGVNIDHIATLRQARGTNYDPVHAAVAEHAGAEGITIHLEDRRHIIDRDVYT	60
Query	61	LRQTL DTRMNLEMAVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC	120
		L +TL TRMN EMAVTEEML IA + KP + CLVPEKR+E+TTEGGLDVAGQ+DK+ A	
Sbjct	61	LAKTLKTRMNFEMAVTEEMLDIACDIKPAYVCLVPEKREELTTEGGLDVAGQQDKIAAAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		RL GI+VSLFIDAD+ QI AA VGAP IEIHTGICYADA+TDAEQA EL RI + AT	
Sbjct	121	ARLTQEGIKVSLFIDADKAQIDAAVAVGAPVIEIHTGICYADAETDAEQATELQRITEMAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A GL VNAGHGL YHNVKIAAAIPE++ELNIGHAII RA + GL AV +MK+LMLE	
Sbjct	181	YAHGKGLVVNAGHGLHYHNVKIAAAIPELYELNIGHAIIARAAIDGLATAVRDMKQLMLE	240
Query	241	AR 242	
		^R	
Sbjct	241	GR 242	

>ref|YP_001093187.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella PV-4]

gb|ABO22928.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella loih PV-4]
Length=245

GENE ID: 4921109 Shew_1057 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella loihica PV-4]

Score = 329 bits (844), Expect = 1e-88, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 200/242 (82%), Gaps = 0/242 (0%)

Query	1	MAELL LGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI	60
		M+ + LGVNIDHIATLR ARG T+YDPDV AA +AE AGA+GITVHLREDRRHI DRD+ +	
Sbjct	1	MSRIHLGVNIDHIATLRQARGTSYPDPVHAAVAEHAGAEGITVHLREDRRHICDRDIYL	60
Query	61	LRQTL DTRMNLEMAVTEEMLAI AVETKPHFCCLVPEKRQEVTTTEGGLDVAGQRDKMRDAC	120
		L +T+ TRMN EMAVT+EML IA E KP + CLVPEKR+E+TTEGGLDVAGQ+DK+R A	
Sbjct	61	LAKTIKTRMNFEMAVTDEMLDIACEVKPAYVCLVPEKREELTTEGGLDVAGQQDKIRAAV	120
Query	121	KRLADAGIQVSLFIDADEEQIKAAA EVGAPFIEIHTGICYADAKTDAEQAQELARIAKAAT	180
		+RL GI+VSLFIDAD QI A VGAP IE+HTGICYADA+TDAEQA+ELARI + AT	
Sbjct	121	ERLTALGIKVSFLFIDADPVQIDATVAVGAPVIELHTGICYADAETDAEQAKELARITEMAT	180
Query	181	FAASLGLKVNAGHGLTYHNVKIAAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE	240
		+A GL VNAGHGL YHNVKIAAAIPE++ELNIGHAII RA + GL AV +MK+LM+E	
Sbjct	181	YAHGKGLVVNAGHGLHYHNVKSIAAAIPELYELNIGHAIIARAAIDGLKAVRDMKQLMVE	240
Query	241	AR 242	
		^R	
Sbjct	241	GR 242	

>ref|YP_001759633.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella ATCC 51908]

gb|ACA85538.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella wood ATCC 51908]
Length=245

GENE ID: 6115481 Swoo 1246 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella woodyi ATCC 51908]

Score = 329 bits (844), Expect = 1e-88, Method: Compositional matrix adjust.
Identities = 171/242 (70%), Positives = 197/242 (81%), Gaps = 0/242 (0%)

```
Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ +LLGVNIDHIATLR ARG+YDPDV AA +AE AGA+GITVHLREDRRHI DRD+ +
Sbjct 1 MSRIILLGVNIDHIATLRQARGTSYPDPVHAAVAEHAEGITVHLREDRRHIVDRDIYL 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
      L +TL TRMN EMAVT+EML IA E KP + CLVPEKR+E+TTEGGGLDVAGQ K+ A
Sbjct 61 LAKTLKTRMNFEMAVTDEMLDIACEVKPAYVCLVPEKREELTTEGGGLDVAGQMGKIESAV 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
      +RL D G++VSLFIDAD+ QI AA VGAP IEIHTGICYADA DA+QA+ELARI + AT
Sbjct 121 QRLTDIGVKVSLFIDADKTQIDAAVAVGAPVIEIHTGICYADATNDADQAKELARITEMAT 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI RA + GL AV +MK+LM E
Sbjct 181 YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIARAAIDGLATAVKDMKQLMNE 240

Query 241 AR 242
      R
Sbjct 241 GR 242
```

>ref|YP_870654.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp ANA-3]

gb|ABK49248.1 | **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. ANA-3]
Length=245

GENE ID: 4478566 Shewana3_3023 | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella sp. ANA-3]

Score = 329 bits (843), Expect = 1e-88, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 194/242 (80%), Gaps = 0/242 (0%)

```
Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ +LLGVNIDHIATLR ARG+YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MSRIILLGVNIDHIATLRQARGTSYPDPVHAAA+AEHAGADGITIHLREDRRHIDRDVYL 60

Query 61 LRQTLDTMRNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTTEGGGLDVAGQORDKMRDAC 120
      L +TL TRMN E AVTEEML IA E KP + CLVPEKRQEVTTTEGGGLDVAGQ DK+ A
Sbjct 61 LAKTLKTRMNFECVTEEMLNIAACEVKPTYVCLVPEKRQEVTTTEGGGLDVAGQLDKITA+V 120

Query 121 KRLADAGIQVSLFIDADEEQIKAAAEVGAFFIEIHTGICYADAKTDAEQAQELARIAKAAT 180
      RLA IQVSLFIDAD+ QI AA GAP IEIHTGICYADAKT E+A+ELARI++ A
Sbjct 121 SRLAANRIQVSLFIDADKTQIDAAVAAAGAPLIEIHTGICYADAKTAEELAKELARISEMAK 180

Query 181 FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE 240
      +A GL VNAGHGL YHNVK IAAIPE++ELNIGHAI RA + GL AV +MK LMLE
Sbjct 181 YAHGKGLVVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKALMLE 240

Query 241 AR 242
      R
Sbjct 241 GR 242
```

>ref|NP_716971.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewanella on MR-1]

sp|Q8EH78.1|PDXJ_SHEON RecName: Full=Pyridoxine 5'-phosphate synthase; Short=PN
gb|AAN54416.1|AE015579_5 | **G** pyridoxal phosphate biosynthetic protein PdxJ [Shewa MR-1]
Length=245

GENE ID: 1169172 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Shewanella oneidensis MR-1] (10 or fewer PubMed links)

Score = 328 bits (842), Expect = 2e-88, Method: Compositional matrix adjust.
Identities = 174/242 (71%), Positives = 193/242 (79%), Gaps = 0/242 (0%)

```
Query 1 MAELLLGVNIDHIATLRNARGTAYPDPVQAAAFIAEQAGADGITVHLREDRRHITDRDVRI 60
      M+ +LLGVNIDHIATLR ARG+YDPDV AA +AE AGADGIT+HLREDRRHI DRDV +
Sbjct 1 MSRIILLGVNIDHIATLRQARGTSYPDPVHAAA+AEHAGADGITIHLREDRRHIDRDVYL 60
```

```

Query   61   LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC   120
Sbjct   61   LAKTLKTRMNFEC AVTEEM LNIACEVKPTYVCLVPEKRQEVTTTEGGLDVAGQLDKITAAV   120

Query   121  KRLADAGIQVSLFIDADEEQIKAAAEV GAF FIEIHTG CYADAKTDAEQAQELARIAKAAT   180
Sbjct   121  SRLAANGIQVSLFIDADKTQIDAAVASGAPLIEIHTG CYADAKTAD EEAKELE RIREMAK   180

Query   181  FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
Sbjct   181  YAHGKGLIVNAGHGLHYHNVKPIAAIPELYELNIGHAIVARAAIDGLATAVKDMKTLMLE   240

Query   241  AR   242
Sbjct   241  GR   242

```

>ref|YP_942095.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Psychromonas 37]
gb|ABM02496.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Psychromonas in 37]
Length=244

GENE ID: 4626841 Ping_0643 | pyridoxal phosphate biosynthetic protein PdxJ [Psychromonas ingrahamii 37]

Score = 328 bits (840), Expect = 3e-88, Method: Compositional matrix adjust.
Identities = 162/242 (66%), Positives = 192/242 (79%), Gaps = 0/242 (0%)

```

Query   1   MAELL LGVNIDHIATLRNARGTAYPDPVQAA FIAEQAGADGITVHLREDRRHITDRDVRI   60
Sbjct   1   MSQILLGVNIDHIATLRNARGTCYPEPAHLAAIAECAGADGITIHLREDRRHINDRDVAV   60

Query   61   LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC   120
Sbjct   61   LAQTLQTRM NLEMAVTDEMVDIALKTKPAFVCLVPEKREELTTEGG LNVVASFSKIASAV   120

Query   121  KRLADAGIQVSLFIDADEEQIKAAAEV GAF FIEIHTG CYADAKTDAEQAQELARIAKAAT   180
Sbjct   121  SRLNAAAIQVSLFIDPEN AQIDAAIKTGAA YIELHTG KYADAPSEDIQQFELMRVAKAAT   180

Query   181  FAASLGLKVNAGHGLTYHNVKAI AAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLE   240
Sbjct   181  YASQAGIKVNAGHGLNYHNVKPIAALPEI IELNIGHAIVARALVDGFGPAVAEMKRLMVE   240

Query   241  AR   242
Sbjct   241  GR   242

```

>ref|YP_693348.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Alcanivorax b SK2]

sp|Q0VP22.1|PDXJ ALCBS **G** RecName: Full=Pyridoxine 5'-phosphate synthase; Short=
emb|CAL17076.1| **G** pyridoxal phosphate biosynthetic protein PdxJ [Alcanivorax bo SK2]
Length=244

GENE ID: 4212451 pdxJ | pyridoxal phosphate biosynthetic protein PdxJ [Alcanivorax borkumensis SK2] (10 or fewer PubMed links)

Score = 328 bits (840), Expect = 3e-88, Method: Compositional matrix adjust.
Identities = 163/238 (68%), Positives = 187/238 (78%), Gaps = 0/238 (0%)

```

Query   1   MAELL LGVNIDHIATLRNARGTAYPDPVQAA FIAEQAGADGITVHLREDRRHITDRDVRI   60
Sbjct   4   MSRVLLGVNIDHIATLRQARGTRYPEPVQAALVAEQAGADGITVHLREDRRHINDRDVEL   63

Query   61   LRQTL DTRM NLEMAVTEEM LAIAVETKPHFCCLVPEKRQEVTTTEGGLDVAGQ RDKMRDAC   120
Sbjct   64   LAQTLQTRM NLEMAATEEMVVIACRIQPPHCCLVPEKREELTTEGG LDDVVGNKAWIAQCC   123

Query   121  KRLADAGIQVSLFIDADEEQIKAAAEV GAF FIEIHTG CYADAKTDAEQAQELARIAKAAT   180
Sbjct   124  QRLGQAGIEVSLFIDAEESQILAARECGAPAIEIHTGGYADAQTIDQQQQELARIRSAVA   183

```

Query	181	FAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLM	238
		FA + GL VNAGHGL YHN AIA IP ++ELNIGH+II RA +TGL +AV M+ L+	
Sbjct	184	FALAQGLIVNAGHGLHYHNTLAIAEIPGINELNIGHSSIARAATGLDEAVRSMRSL	241

Select All [Get selected sequences](#) [Distance tree of results](#)